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### **SEARCH REQUEST FORM**

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Search Topic: Please write a detailed statement of that may have a special meaning. Ga copy of the sequence. You may	ive examples or relevant citatio	ns, authors keywords,	ject matter to be searched. Define any terms etc., if known. For sequences, please attach claim(s).
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4, 2003, 17:30:47; Search time 2758 Seconds (without alignments) 10562.693 Million cell updates/sec

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4109280 Total number of hits satisfying chosen parameters:

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Listing first 45 summaries

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PLN 11-SEP-2001

REFERENCE AUTHORS TITLE

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 10934)
Haese, A., Schubert, M., Herrmann, M. and Zocher, R.
Molecular characterization of the enniatin synthetase gene encoding a multifunctional enzyme catalysing N-methyldepsipeptide formation

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4 (bases 1 to 10934)
4 (bases 1 to 10934)
5 (bases 2 to 10934)
Discher,R. (bases 2 to 10934)
Direct Submission
Submitted (11-SEP-2001) Zocher R., Technische Universtaet Berlin, Max. Volmer- Institut fuer Biophysikalische Chemie und Biochemie und Molekulare Biologie Sek. OE2, Franklinstr. 29, D-10587 Berlin, GERMANY
On Sep 12, 2001 this sequence version replaced gi:7327885.
Location/Qualifiers
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Submitted (22-MAR-2000) Zocher R., Technische Universtaet Berlin,
Max- Volmer- Institut fuer Biophysikalische Chemie und Biochemie,
Abteilung Biochemie und Molekulare Biologie Sek. OE2, Franklinstr.
29, D-10587 Berlin, GERMANY
Revised by [5]
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Submitted (24-NOV-1992) Haese A., Technische Universtaet Berlin,
Institut fuer Biochemie u. Mol. Biologie, Franklinstr.29, W-1000
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in Fusarium scirpi
Mol. Microbiol. 7 (6), 905-914 (1993)
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Zocher, R.
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                                                       TTGGAAGATTCAAGTTCCAGGGTCTCGAGTCCGTACCTGTGCCTAGCAAAGCGTACACTC 714
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"Indo.N., Okakura, K., Miyamoto, K., Watanabe, M., Yanai, K.,
Yasutake, T., Alhara, S., Futamura, T., Kleinkauf, H. and Murakami, T.
Cyclic depsipeptide synthetase and its gene and mass production
system of cyclic depsipeptide
system of cyclic depsipeptide
Batton: Wo 0118179-A 1 15-MAR-2001,
MEJJ SEIKA KAISHA LTD, NAOKI MIDO, KAORU OKAKURA, KOICHI MIYAMOTO,
MANABU WATANABE, KOJI YANAI, TETSUYA YASUTAKE, SATO AIHARA, AKAEUMI
OS Mycella sterilia
DN WO 0118179-A/1
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Cyclic depsipeptide synthetase and its gene and mass production
system of cyclic depsipeptide.
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                        GATTTGACATGGAGTTCCATCTGTTTCAAGAAACCGACAGCCTTAAAGGTAGCGTCAACT
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07-SEP-2000 WO 2000JP006103
07-SEP-1999 JP 99P 253040,06-APR-2000 JP 00P 104291
MIDO,KAORU OKAKURA,KOICHI MIYAMOTO,MANABU WATANABE, PI
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peptide synthetase for PF1022
Key Location/Qualifiers
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(13). .(9630).
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unidentified.
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Pred. No. 1.6e-102;
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RESULT

DB 6; Length 9633;

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                                     TCTGCAACGAACACAACACGACCTCTTTCGTCGTTCTTCTAGCTGCGTTCCGTGCCGCTC
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Sordariales; Chaetosphaeriaceae; mitosporic Chaetosphaeriaceae;
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Unpublished
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Submitted (12-MAR-1996) F. Bernhard, Freie Universitaet
Institute of Crystallography, Takustr. 6, 14195 Berlin,
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Cylindrotrichum oligospermum.
Cylindrotrichum oligospermum
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Bernhard, F.
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Bernhard, F.
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MEIJI SEIKA KAISHA LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1999 JP 99P 253040,06-APR-2000 JP 00P 104291
NAOKI MIDO,KAORU OKAKURA,KOICHI MIYAMOTO,MANABU WATANABE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9633 BP; 2318 A; 2834 C; 2462 G; 2019 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TETSUYA YASUTAKE, SATO AIHARA, TAKAFUMI FUTAMURA, HORST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.2%; Score 392; DB 23;
63.3%; Pred. No. 1.6e-102;
tive 0; Mismatches 360;
                                                                                                               Created)
Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C12N9/00, C12N15/52, C12N1/15, C12P21/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
                  BP.
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                 standard; DNA; UNC; 9633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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(13). .(9630)
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07-SEP-1999 JP 99P 25304
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Best Local Similarity 63.39
Marches 637; Conservative
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                                                                                                              08-FEB-2002 (Rel. 70, 08-FEB-2002 (Rel. 70,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycelia sterilia
JP 03075848-T/1
06-MAR-2001
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                                                                                                                                                                                                                JP 03075848-T/1
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                                                BD010088;
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                                                                   2136 TICTACATCACGTCCTAGACCAGCCTCACACCCCGATTACTTCCCTTCCGCTCGCGAATG
                                                                                                                                    895 GCATTGTGACTCTTGAAAAATTGGATGTTCTCAACGTCAAACATGTCGACTATCCCCGAG
                                                  CATTCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTGGATCCA
                                                                                                                 GAGATCTGTCAAGCACCTCTCGCACAACTCATTTTTGCAGTGCACTCACAGAAGGACC
                                                                                                                                                                                TTGGAAGATTCAAGTTCCAGGGTCTCGAGTCCGTACCTGTGCCTAGCAAAGCGTACACTC
                                                                                                                                                                                                                                               GATITGACATGGAGTICCATCIGITICAAGAAACCGACAGCCTIAAAGGIAGCGICAACI
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 46899;
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/strain="AFTCC 34921"
/db_xref="taxon:29910"
a 13511 c 12510 g 10227 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 339.4; DB 6
Pred. No. 3.6e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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A36768
A36768.1 GI:2294035
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60.1%;
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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EQTSSFDLASEPGWRVSLLRIANNDHVLSIVMHHIISDGWSIDLIRRELGQLYSAALR
GYDPGSQLSPLPIQYRDFSVWQKQAEQYAEHERQLEVWTTRADDSPAELLTDDLRPT
VLSGNAGVQULAIDGSLYEKLRAFCRAYGTTSFAVLLAAFRATHYRLTGAEDATIGTP
IANRNRFELBRLIGFEVNTQCMRITVDRDDTFETLMQQVRSTTTAAFANQDVPFERIV
SALLPGSRDTSRNPLVQLMFVLHSQKDLGMIQLEGPVPTAASTRFDLEFHLFQE
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                                                                                                                                                                                                                                                                              LPSYMVPARITILDQMPLNANGKVDRKDLARRAQTVSKAEKLPSARVAPRNEVEVVLC
EEFSDVLGVEVGVADSFFDLGGHSLMATKLAARISRRLNARVSVKEVFDQPVLADLAI
VIQRGSKPHNPILTAPYSGPVEQSFAQGRLWFLDQINLGASWYLMPLAVRLRGPLHTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGSDVAAPKVRVQDVEMVRVDDTLGYDILDDŸANSAVRPSPTSLAYVMFTSGSTGKPK
GVMIEHRAVLRLVKNSNVVSILPMTPRVAHLSNLGFDISVQEVYTALLNGGTLVCIDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1656 ACTACCGCCTCACAGGCGCCGAAGACGCCACCATTGGTACGCCCATTGCCAACCGGAATC 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="DPQQQLVPVGVMGELVVTGDGLARGYTDPVLDQGRFVQIRIKGE
                                                                                                                                                                                                                                             SVRAYRTGDRARYRPKDGQIEFFGRMDQQIKIRGHRIELAEVEHAMLHHDAVRDAVVV
IRLQGDQEPEMIGFVVVRADETVQQDLSRTHGAVNSANWEEQFEIQTEKEIRNRLQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                            LLDIERSDYPRESSLVDVFREQVAACPDATAVIDSSSRLTYTQLDRQSDEVAGWLRRR
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                                                                                                              /function="amino acid adenylate forming module"
/note="SDZ 214-103"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                /organism="Cylindrotrichum oligospermum"
/strain="NRRL 18230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 380;
                                                                                                                                                            /product="peptolide synthetase"
/protein_id="CAA65395.1."
/db_xref="GI:1770180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 360; DB 8;
Pred. No. 2.9e-93;
                                                                                                                                                                                                               /db_xref="SPTREMBL:P97961"
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                                                                /db_xref="taxon:72418"
/clone_lib="pCB11"
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Location/Qualifiers
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ilarity 61.3%;
Conservative
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617; Conserv
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                                                                                                                                                                      Length 46899
                                                                                                                                                                                   Pred. No. 3.6e-87;
0; Mismatches 391; Indels
                                Unclassified.

1 (bases I to 46899)
Leitner,E., Schneider,E., Schoergendorfer,K. and Cyclosporin synthetase
Patent: US 5827706-A 1 27-OCT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                         DB
                                                                                                                                                                        Score 339.4;
                                                                                                                                10227
                                                                                                                  /organism="unknown"
13511 c 12510 g
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Best Local Similarity 60.1%;
Matches 603; Conservative (
                                                                                                         .46899
           Unknown.
Unclassified.
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Unknown.
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FEATURES
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        ACCCGCTGTCACCTCCTCTACCTATCCAGTACAGCGACTTTGCAAATGGCAGA
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TTGACATGGAGTTCCATCTGTTTCAAGAAACCGACAGCCTTAAAGGTAGCGTCAACTTTG

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29-SEP-1999

linear

DNA

Sequence 1 from patent US 5827706. AR050554 AR050554.1 GI:5973279

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 6 AR050554 LOCUS

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CCGATGAGCTGTTCAAAATGGAGACTGTTGAAAATGTCGTCAGAGTATTCTTTGAGATTC

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Submitted (29-NOV-1993) Weber G., Biochemie Ges. m.b.H., Molekulare
Genetik 2, Kufstein-Schaftenau, Austria, A-6330
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SEPAVHVKTMPLTDGLAAIRDMGLLDIGTTDYPREASVVDMFGEQVALNPSATAVADA
SSRLSYSELDHKSDQLAAWLRRRQLKPETLIGVLSPPSCETMVSFLGILKAHLAYLPL
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LADLAATIQRGSTLYSVIPTTEYTGPVEQSFAQGRLWFLEQLNTGASWYNVMLTVRLR
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LLAAFRVAHFRLTGAEDATIGAPVANRDRPELENMVAPLATLQCMRVVLDEDDTFESV
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Weber, G., Schorgendorfer, K., Schneider-Scherzer, E. and Leitner, E. The peptide synthetase catalyzing cyclosporine production in Tolypocladium niveum is encoded by a giant 45.8-kilobase open
TGAGAAACGGGCTTCAAAGTTCGCGGACACCAGTCTCAATACTTCCTTTGACTGATGGCA
                                                 TTGTGACTCTTGAAAAATTGGATGTTCTCAACGTCAAACATGTCGACTATCCCCGAGAAT
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niveum (ATCC34921) simA gene for cyclosporine synthetase.
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/strain="ATCC34921"
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885. .46730
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VERSION
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AUTHORS
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LTDGTLQDGPTIERPSAQSLAYAMFTSGSTGRPKGVMYQHRNIVRLVKNSNVVAKQPA AARIAHISNLAFDASSWEIYAPLLNGGAIVCADYFTTIDPQALQETFQEHEIRGAMLP PSLLKQCLVQAPDMISRLDILFRAGDRFSSVDALQAQRLVGSGVFNAYGPTENTILST PFEQVVSSLMPSSSRDASRNPLVQLMFALHGQQDLFKIQLEGTEEEVIPTEEVTRFDI EFHLYQGASKLSGDIIFAADLFEAETIRGVVSVFQEVLRRGLQQPQTPIMTMPLTDGI PELERMGLLHMVKTDYPRNMSVVDVFQQQVRLSAEATAVIDSSSRMSYAELDQRSDQV YVMDQNQQLVPLGVMGELVVTGDGLARGYTNPALDSDRFVDVIARGQLLRAYRTGDRA RYRPKDGQVEFFGRMDHQVKVRGHRIELAEVEHALLSSAGVHDAVVÝSNSQEDNOGVE MVAFITAQDNETLQEAQSSNQVQEWESHFETTAYADITAIDONTLGRDFTSWTSMYDG TLIDKREMQEWLDDTWRTFLDGQAAGHVLEIGTGTGMVLFYJGGAGLKSYIGLEPSQS KINAESWIDFASSQMDRQGLARLLKENKDAESIAVFNIPYSKTIVERHIAKSLADDHD GDDTHSSIDGVAWISAAREKASQCPSLDVHDLVQLAEDAGFRVEVSWARQRSQNGALD DTTEHNPILPTSYTGPVEQSFAGGRLWFLDQLNVGATWYLMPFAVRLRGPLVVSALAA ALLALEERHETLRTTFIEQEGIGMQVIHPFAPKELRVIDVSGEEESTIQKILEKEGTT PFNLASEPGFRLALLKTGEDEHILSTVMHHAISDGWSVDIFQQEIGQFYSAILRGHDP RAGEIPVVVDGLIYEKLQDFCRIRQVTAFTVLLAAFRAAHYRMTGTEDATIGTPIANR NRPELEGLIGFFVNTQCMRITVDVEDSFETLVHQVRETTLAAHANQDVPFEQIVSNIL QQTDY PCDASVVQIFKQOVAVNPDYIAVRDESTRLSYADLDRKSDQVACWLSRRGIAP ETFVAILAPRSCETIVAILGVLKANLAYLPLDVNVPASRLEAILSEVSGSMLVLVGAE TPIPBGMAEAETIRITEILADAKTDDINGLAASQPTAASLAYVIFTSGSTGRPKGVWV MGELIVTGDGLARGYTTSSLNTGRFINVDIDGEQVRAYRTGDRVRYRPKDLQIEFFGR IDHQVKIRGHRIEPAEVEYALLSHDLVTDAAVVTHSQENQDLEMVGFVAARVADVRED FGDMRSHAINRDFLVARAVHALGDKATKAEIQREVVRMEESEDELLVUPAFFTSLTTQ VENIKHVEILPKRMRATNELSSYRYAAVLHVNDLAKPAHKVSPGAWVDFAATKMDRDA LIRLERGTKISDHIAIANIPNSKTIVERTICESVYDLGGDAKDSNDRVSWLSAARSNA AQGRLWFLDQLNFGATWYLMPLAVRLRGAMNVHALTĀALLALERRHELLRTTFYEÖNG VGMQKVNPVVTETLRIIDLSNGDGDYLPTLKKEQTAPFHLETEPGWRVALLRLGPGDY ILSVVMHHIISDGWSVDVLFQELGQFYSTAVKGHDPLSQTTPLPIHYRDFALWQKKPT QESEHERQLQYWVEQLVDSAPAELLTDLPRPSILSGQAGEMSVTIEGALYKNLEEFCR VHRVTSFVVLLAALRAAHYRLTGSEDATIGTPIANRNRPELEQIIGFFVNTQCIRITV FQEILRRGLNGPDVPISTLPLQDGIVDLQRQGLLDVQKTEYPRDSSVVDVFHEQVSIN PDSIALIHGSEKLSYAQLDRESDRVARWLRHRSFSSDTLIAVLAPRSCETIIAFLGIL QGLTSDMAVINSVAQYFPTPEYLAETIKSLVQVPGMKRIYLGDMRSWAMNRDFAARRA AYSLADNASKDRVRQKMMELEEKEEELLVDPAFFTALASQLQDRIQHVEILPKRMKAT NELSSYRYAAVLHISDEPLPIYKIDPEAWINFEGSRLTREALAQVLKENENAESVAIS NIPYSKTVVERHIVRSLDQEDANAPEESMDGSDWISAVRTRAQQCHTLSASDLFDIAE ATIGVPSANRNRPELENVIGFFVNTQCIRITIDENDNFESLVRQVRSTTTAAQDNQDV **AAWLROROLPAETFVAVLAPRSCEAVIALFGILKAGHAYLPLDVNVPAARLRAILAEV** KGEKLVLLGAGEPSPEGOSPEVSIVRIADATSPAGHASLRDGKSKPTAGSLAYVIFTS GSTGKPKGVMIEHRGVLRLVKQTNILSSLPPAQTFRMAHMSNLAFDASIWEVFTALLN GGSLVCIDRFTILDAQALEALFLREHINIALFPPALLKQCLTDAAATIKSLDLLYVGG DRLDTADAALAKALVKSEVYNAYGPTENTVMSTLYSIADTERFVNGVPIGRAVSNSGV AVQFVNKAAQTFPGLEGKAQVHVGTAMDTGRLSALSPDLIVINSVAQYFPSREYLAEV **VEALVRIPGVRRIFFGDMRTYATHKDFLVARAVHTNGSKVTRSKVQQEVARLEELEEE** LLVDPAFFTSLKESLSEEIEHVEILPKNMKVNNELSSYRYGAVLHIRNHNQNQSRSIH VFFHHFQPTENESRALVDFPTDYKGQQARSLTNRPLQRVESRRIEAQVREQLQVLLPA YMIPARIVVLQNMPLNTSGKVDRKELTLRAKVTAARTPSSELVAPRDSIEAIICKEFK DVLGVEVGITDNFFNVGGHSLLATKLAARLSRQLNAQIAVKDIFDRPVIADLAATIQQ LAQIAPLSIQYRDFATWQRQIFQVAEHRRQLAYWTKQLADNKPAELLTDFKRPPMLSG NGSIVYAADLEVPETIQSVITIFQGILQKGLGEPDMPVASMALDGGLESLRSTGLLHP EHRGIVRLTKQTNITSKLPESFHMAHISNLAFDASVWEVFTTLLNGGTLVCIDYFTLL ESTALEKVFFDQRVNVALLPPALLKQCLDNSPALVKTLSVLYIGGDRLDASDAAKARG LVQTQAFNAYGPTENTVMSTIYPIAEDPFINGVPIGHAVSNSGAFVMDQNQQITPPGA ESSNQVQEWQTHFDSIAYADITTIDQQSLGRDFMSWTSMYDGSLIKKSQMQEWLDDTM RSLLDSQPPGHVLEVGTGTGMVLFNLGREGGLQSYVGLEPSPSATAFVNKAAKSFPGL EDRIRVEVGTATDIDRLGDDLHAGLVVVNSVAQYFPSQDYLAQLVRDLTKVPGVERIF **VKVASLSAIDLVDIAQEAGFRVEISCARQWSQNGALDAVFHHLGPSPQSSHVLIDFLT** DHOGRPEEALTNHPLHRAOSRRVEROIRERLOTLLPAYMIPAOIMVLDKLPLNANGKV DRKQLTQRAQTVPKAKQVSAPVAPRTEIERVLCQEFSDVLGVDIGIMENFFDLGGHSL MATKLAARISRRLETHVSVKEIFDHPRVCDLVLIVQQGSAPHDPIVSTKYTGPVPQSF NEDETFESLVQQVRSTATAAFAHQDVPFEKIVSTLLPGSRDASRNPLVQLMFAVHSQK NLGELKLENAHSEVVPTEITTRFDLEFHLFQQDDKLEGSILYSTDLFEAVSVOSLLSV IYNVAENDSFVNGVPIGSAVSNSGAYIMDKNQQLVPAGVMGELVVTGDGLARGYMDPK PGSSDTSRNPLVOLMFALHSOONLGKVRLEG1EEE11S1AETTRFD1EFHLYQEAER1 KANLAYLPLDVKAPAARIDAIVSSLPGNKLILLGANVTPPKLQEAAIDFVPIRDTFT

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I ETAILRDEFEDVIGTEVSVLDNFPDIGGHSLMATKILAARVSRRLDAHI SI KUVFDOPV
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LEVLRREQTVPPDLSSEPEGWYCL VYRGEDHVLS I VMHHI I I YDGWSVDI LRGELGOF
YSAALRGOPPLLHAANDLPIOYRDFAAWOREKKQVEBHOROLGYWSKOLVDSTPAELLT
DLPRRSI ILSGRAGSVDVI I EGSVYGALQSFCRRRSVTTFVVLLTVRRI HAFRLA VDD AQLDQQSDRLAIWLSRRHMMPETLVGVIAPRSCETIIAMFGIKKANLAYLPLDINSPA ARLRSILSAVDGNKLVLLGSGVTAPEQENPEVEAVGIQEILAGTGLDKTQGSNARPSA SLAYVIFSGSTGKRKGVWPEHRSYTRLAKDSNVISKLPQGARVAHLANIAEDASIW EIATTLINGATLVCLTOVHTVLDGYTKKEVENSTITVVTLHMALLKQGVAEIPETLAH LDLLYTGGDRVGGHDAMRARSLVKIGMFSGYGPTENTYTSTIYEVDADEBHFVNGVPIG KTVSNSGAYVMDRNQLVPSGVVGELVVTGDGLARGYTDPSLNKNRFIYITVUGESIR AYRTGDRVRYRPHDLOIEFGRMDQOVKIRGHRIEPGEVESALLSHNSVQDAAVVICA BADOBSGABWYARVARANTEDDEDTQEESAVDOVGMETHFERAXSEVKDIRGSEVGN DFMGMTSMYDGSEIDRYDMHENDLIDAREDENDGETGHTGATGTGTGWWFNLAKCPG LQGYVGFEPSKSAAQFVNDAAOSFPALKDGRSIVHVGTATDINKAGPIQPRLVVINSV RQWYFPEPLLENVEALVOIPSYERTYFGDMRTNAINRDFVASRALHTLGEKANKRLV RQWYFELANEELLYBRYDFATSLFRYRGDMRTNAINRDFVASRALHTLGEKANKRLV VRGSREQSTIHQVSPNANDFPADGLDRQTLINLLKEBRKDAGTVAIGNIPSSKTYRAVLH IDLSTQPKDAYLAVLKHEQTTLFDLATEPGWRVALIRLGEEEHILSIVMHIIISDGWS
VEVLEPDEMHERYSALKQDDREQILEDLIQYRDFAMQHTEEDVAEHQRQLDYWTEH
VEOSTPAELITDLEPRESILGSRANELPLTIEGRIHDKLRAFCRYNQATPFVILLAALR
AAHYRLTGAEDATLGTPIANRNRPELENMIGFFVNTQCNRIAIEBDDNFESLYRRYRS TATSAFANQDVPFESIVSSLLPGSRDASRNPLVQVITAVHSQQDLGKLTLEGLRDEAV DSAISTRFDVEFHLFEHADRLSGSVLYAKELFKLRTIESVVSVFLETLRRALDQPLTP LAVLPLTDGVGEIASKGLLDVPRTDYPRDANIVEVFQQHVRATPDAIAVKDATSILTY ATIGTPIANRNRPELETLYGCEVNTQCMRISIADDDNFEGLYRQVRNYATAAYANQDV PFERIVSALVPGSRNTSRNPLVQLMFAVQSVEDYDQVRLEGLESVMMPGEASTRFDME FHLVPGDQKLTGSVLXSSDLFEQGTIQNFVDIFQECLRSVLDQPLTPISVLPFSNAIS NLESLDLLEMPTSDYPRDRTVVDLFREQAAICPDSIAVKDSSSQLTYAQLDEQSDRVA AWLHERHMPAESLVGVLSPRSCETIIAYFGIMKANLAYLPLDVYAPDARLAAILDTVE GERLLLLGAGVPQPGIQIPRLSTAYIAEALSHATTVDVTSIPQPSATSLAYVIFTSGS RPRDGQLEFFGRMDQMVKIRGVRIEPGEVELTLLDHKSVLAATVVVRRPPNGDPEMIA FITIDAEDDVQTHKAIYKHLQGILPAYMIPSHLVILDQMPVTDNGKVDRKDLALRAQT VQKRRSTAARVPPRDEVEAVLCEEYSNLLEVEVGITDGFFDLGGHSLLATKLAARLSR ISVRDVFDQPVVADLAAVIQRNSAPHEPIKPADYTGPVPOSFAQGRLWFLDQLNVGAT WYLMPLGIRLHGSLRVDALATAISALEQRHEPLRTTFHEEDGVGVQVVQDHRPKDLRI TGKPKGVMIEHRĞIVRLVRDTNVNVFPESGSALPVSHFSNLAMDATWEITTAVLNGG TVCIDRDYMLDIAALNSTFRKENVPRAAFFTPRETKQCLAFTPELVANLDILHTPAGDR LDPGDANLAGKTAKGTENVLGHTBNTAY STFYPVVGEETFVNGVPGRGISNSHAY IDRHQKLVPAGVMGELILLTGDGVARGYTDSALNKDRFVYIDINGKSTWSYRTGDKARY QLNTRYSVKDVFDQPILADLADIIRRCSHRHDPIPATPYTGPVEQSFAGGRLWFLEQL NLGASWYLMPFAIRWRGPLQTKALAVALNALVHRHEALRTTFEDHDGVGVQVVIQPKSS QDLRIIDLSDAVDDTAYLAALKREQTTAFDLTSEPGWRVSLLRLGDDDYILSIVMHHI FVNKSLSEDDMEEGQNSLDGSAWVAAVRMAAQSCPSLDAMDVKEIAQEAGYQVEVSWA ISDGWTVDVLRQELGQFYSAAIRGQEPLSQAKSLPIQYRDFAWWQRQENIKEQAKQL KWSQQLABASTPCEPLTDLPRRSILSGSBADAYPWJLGGTVYQLLTDFGYHQVTSFSV LLAAFRTAHYRLTGTLAFVGTPANKNRPELEGLIGFFVNTQCMRMAISETFESL VQQVRLTTTEAFANQDVPFEQIVSTLLBGSRDTSRNPLVQVMRALQSQQDLGRTQLEG MTDEALETPLSTRLDLEVHLFQEVGKLSGSLLYSTDLFEVETTRGTVDYFLEITERGL EQPKQRLMAMPITDGITKLRDQGLLTVAKPAYPRESSVIDLFRQQVAAAPDAJAVWDS SSTLTYADLDGQSNKLAHWLCQRNMAPETLVAVFAPRSCLTIVAFLGVLKANLAYLPL DVNAPAARIEAILSAVPGHKLVLVQAHGPELGLTMADTELVQIDEALASSSSGÖHEQI HASGPTATSLAYVMFTSGSTGKPKGVMIDHRSIIRLVKNSDVVATLPTPVRMANVSNL **AFDISVQEIYTALLNGGTLVCLDYLTLLDSKILYNVFVEAQVNAAMFTPVLLKQCLGN** DAAVVLRKPANQEPEMIAFITSQEDETIEQHESNKQVQGWGEHFDVSRYADIKDLDTS TFGHDFLGWTSMYDGVDIPVNEMKEWLDETTASLLDNRPPGHILEIGAGTGMILSNLG VINGYÄÖYFPTSEYLIKVVKAVVEVPSYKRVFFGDIRSQALNRDFLAARAVRALGDNA SKEQIREKIAELEESEEELLVDPAFFVSLRSQLPNIKHVEVLPKLMKATNELSSYRYA AVLHISHNEEEQLLIQDIDPTAWVDFAATQKDSQGLRNLLQQGRDDVMIAVGNIPYSK MPAIISRLSVLFNVGDRLDAHDAVAASGLIQDAVYNAYGPTENGMQSTMYKVDVNEPF VNGVPIGRSITNSGAYVMDGNQQLVSPGVMGEIVVTGDGLARGYTDSALDEDRFVHVŢ IDGEENIKAYRTGDRVRYRPKDFEIEFFGRMDQQVKIRGHRIEPAEVEHALLGHDLVH KVDGLQKYVGLDPAPSAAIFVNEAVKSLPSLAGKARVLVGTALDIGSLDKNEIQPELV

30582 30522 30762 31062 31182 477 357 657 GAAGATTCAAGTTCCAGGGTCTCGAGTCCGTACCTGTGCCTAGCAAAGCGTACACTCGAT 717 TGAGAAACGGGCTTCAAAGTTCGCGGACACCAGTCTCAATAGTTCCTTTGACTGATGGCA 897 63 AGGA-----CCAATTCATAGAGCAGGAGCAACTCAACTACTGGAAGAAGCAACTCA TTGATGTCTTGCGACGCGATCTCAATCAGCTCTACTCAGCTGCGCTCAAAGGACTCAAAAG ACCCGCTGTCAGCACTCACTCCTACCTATCCAGTACAGCGACTTTGCAAAATGGCAGA 30343 AGGAAGCTGCCCAAGTTGCCGAGCATGAGAGGCAGCTCGCGTACTGGGAGAACCAGTTAG ACGCAGGTTGCGTACATGTTACCATCGACGCGAGCTCTACCAGTCCCTTCGAGCCTTCT GCAACGAACACAACACGACCTCTTTCGTCGTTCTTCTAGCTGCGTTCCGTGCCGCTCATT 358 ATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGAC ATCATCACGATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACAGCAT TCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTGGATCCAGAG ATCTGTCAAGCACCTCTCGCACAACTCATTTTTGCAGTGCACTCACAGAAGGACCTTG TTGACATGGAGTTCCATCTGTTTCAAGAAACCGACAGCCTTAAAAGGTAGCGTCAACTTTG CCGATGAGCTGTTCAAAATGGAGACTGTTGAAAATGTCGTCAGAGTATTCTTTGAGATTC 898 TIGIGACTCTIGAAAATIGGAIGTICTCAACGTCAAACAIGICGACTATCCCCGAGAAI 31183 ACTCGGTTGTCGACAGCAGCAGCTGCCAATCC 31225 958 CGAGCTTGGCTGATGTCTTCCAGACCCAAGTCTCTGCTTACCC 1000 298 4 238 718 778 838 64 30403 478 30703 538 598 658 pp δ Db Óγ g ŏ Db δy qq q Dp qq QY δ ò δ qq δy Dp Qγ qq qq g Ω ò ò QQ οy q g QΥ οŻ

RESULT 8 A40406/c LOCUS

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Indels

Score 339.4; DB 8; Pred. No. 3.6e-87; 0; Mismatches 391;

33.9%; 60.1%;

603; Conservative

Local Similarity

Query Match Best Local S: Matches 603;

3973

DNA dq

linear

PAT 05-MAR-1997

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LPKVRDAELPLSYAQQRLWFLDQLEPNSAFYNIPMALRLVGNLNQPALEGSSLLEIIHR
HEALRTNFITVDGKPSQIIQTRREQGTGNREQGTVSIVDFKDLSTNEQEIASKQLARQ
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Kocher, H.P., Schneider-Scherzer, E., Schoergendorfer, K. and RECOMBINANT ALANINE RACEMASE AND GAPDH FROM TOLYPOCLADIUM PAtent: WO 9425606-A 33 10-NOV-1994;
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/note="unnamed protein product"
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HQRGADFDLNLMVMEAQGVLCWQYNTDLFEASTITEMAGHTVTLLEGIVNNPQEQI
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                                                                                                                                                                                                    BCT 15-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoffman, D., Hevel, J.M. and Moore, R.E.
Blorect Submission
Submitted (13 NOV-1999) Chemistry, University of Hawaii at Manoa, 2545 McCarthy Mall, Honolulu, HI 96822, USA
1 (Dases I to 40989)
Blorect Submission
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Cyanobacteria: Nostocales: Nostocaceae; Nostoc. (Dases 1 to 40989)
Hoffmann,D., Hevel,J.M. and Moore R.E. Characterization of the nostopeptolide biosynthetic gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-DEC-1999) Chemistry, University of Hawaii at Manoa, 2545 McCarthy Mall, Honolulu, HI 96822, USA Sequence update by submitter on Dec 13, 1999 this sequence version replaced gi:6538756. Location/Qualifiers
538 TCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTGGATCCA 594
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                              40989 bp DNA linear BCT 15-
GSV224 nostopeptolide biosynthetic gene cluster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4S)-4-methylproline and leucine" /note="peptide synthetase; contains 4 modules"
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1370. 14509
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Unpublished
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AUATOLITOTETWATUS IT MAS. LARLAGGETO ELOGICADO IL RHEALRTREITUDG

QATOLITOTETWATUS IT MAS. LARLAGGETO ELOGICADO IL RHEALRTREITUDG

QATOLITOTETWATUS IT MAS. LARLAGGETO ELOGICADO IL PELATOAL RRATLAVI

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KLSOEGGYTLEWILLAAFDTLLY RYTGTEDILUGSPITANDRSE SIEGLIGFEVITUW

RTDLSGRPSE SELLGRYREMAREA'S SIGHLEPEMIC VARLOPERBLEISHSPLEOVMFYLD

NAPTSGLELTGLIVSSLP IKGTTSREDLTINGNSPTGLIGWEYNTDLFDASTIERU

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GVLLSGGYFRRPETLIEK FINNPFRSRGAGEOGSREFRODRILY

XI VPOKROKLIYSPYRSFLKSKLEPEYNPELLENDELGGGSTRREDTENDTENDEL

KVELPRESEHAAFSTENDELSENSTANDLELGGELGATREDTENDTENDEL

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KVELPRESENDENDELTLEK FINNPFRSRGAGEOGSREFROMERLY

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GINCTLSVVDFRKELYNATURAGOLVORDOLALLY

TULAABAPTLLERTYTATARZOGLYKOPOLALLY

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Length 40989; 12; Indels 10.6%; Score 106.2; DB 1; 52.5%; Pred. No. 2.5e-19; ive 0; Mismatches 268; Conservative Similarity Local Simines 309; Query Match Best Loca Matches

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KVAAVTPDLERLLAIVTTLDLAVAKARYSLWIGSNPPRFINRODNEIITLRNLRHPLL
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complement(6817. 8550)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MYFLPVLQTDTVIILNLASVREGNLDVYIDENIDNVIKTFGNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEVVRLQAGAEDTLHAWKLLCEQSRQEFQIIYDLLNVELIERGESFYNPLLPKVVENL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative arginyl-tRNA synthetase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative patatin-like protein"
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9359.
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                                                                                                                                                                                                                                                                                                                                         2320. .4077
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                                                                                    5334 CTTTECTGGTGCATATCAAAGTTTGCCCTCTCTGCTGAACTCACTGGTAGGTTGACAC 5393
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5692
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Submitted (06-APR-2000) Paulin L., Institute of Biotechnology,
University of Helsinki, P.O.Box 56, 00014 University of Helsinki,
FINLAND
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                                                                                                                                                                                                                                                                               292 CCTTCTGCAACGAACACAACACGACCTCTTTCGTCGTTCTTCTAGCTGCGTTCCGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                        5634 AGGCATATTCGCATCAGCATTTGCCTTTTGAAATGCTAGTGGAAGCATTGCAGCAGAA-
                                                                                                                                                                                                                                                                                                                                3394 AACTGAGTCAGAAACAAGGGGTGACTTTGTTCATGACACTTTTGGCAGCGTTTGATACCT
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Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB
gene, adpC gene, adpD gene, adpE gene and adpF gene.
AJ269505
                                                                                                                                                                232 CTGGAGACGCAGGTTGCGTACATGTTACCATCGACGGCGAGGTCTACCAGTCCCTTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 CAGCATTCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTGGAT
                                                    adpp
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1 (bases 1 to 39436)
Rouhiainen, L., Paulin, L., Suomalainen, S., Hyytiainen, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --CGGGATCTTAGCCATACACCGCTATTCCAAGTGATGTTTACACTTCA 5739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 CCAGAGATCTGTCAAGCACCTCTCGCACAACTCATTTTGCAGTGCA 640
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Genes encoding synthetases of cyclic depsipeptides, anabaenopeptilides, in Anabaena strain 90
MMOL. Microbiol. 37 (1), 156-167 (2000)
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complement(<1. .1657)
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Paulin, L.
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Anabaena sp. 90
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AUTHORS
TITLE
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ASP269505
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DRVLQFASESFDVAAEEIFPTWYKGATVVLRPTQMFPDFASLSQFIAQESLSYLNITP
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PTEEMLAAOHLVAEVENGAVGIHDNFFELGVHSYWQRNWYPASVPLPVELPLSLFAAA nfordavav lfenqultygelntqanqlahhlqslgvrpevlygiylerslsiivtll Allkagggyvpldpdytqqrladisedsqfsvlitqqkllnslpvqgvkiivldtese TGAQLADLIGQSQRQNLEITVPPILPRAENAELSLSYAQQRLWFLDQLQPNSSLYNIP LALRLAGFLEVAALEQSLEEIIYRHEALRTNFITIDGKPTQIIQTVRNWQLSVIELQH LPRLEQETSAQELAITQAIQPFDLASGSLLRATLVVLSETEHILLICMHHIVSDEWSM GVFTQELATSYNAYAGGGSANTAPLPIOYADFAIWORQWLVGEVLQSQLSYWKQOLKD AYRTGSLEPTORPPAVOKTSCAYQEFRALELETOGALMOLSQOGVTLENTLAREPDT AYRTGSOLIVORPPIANRHISEIEGLIGFFVNTLVMRTDLSADPSFSSLLGRYREMA LSAYAHQDLPFEMLVBALQPQRNLSHTPLFQVAFVFQNAPNŞQVELTGLIVSPLVVEA MLTNOSQVNPVSEVKPENLACLLYTSGSTGKPKGVMLTHAALVNHSSAISEVFGLTSG

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TGCAACTGAGTCAGCAACAAGATTGTACTCTGTTTATGACGCTGTTGGCAGCGTTTGATA 13691
                                                                                                                                                                                                                                                                                                                                                                                                                      GCAACCGACCTGAACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 CAGCAGCATTCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTG 588
                                                                                                                                                                                                                                                  289 GAGCCTTCTGCAACGAACAACAACGACCTCTTTCGTCGTTCTTCTAGCTGCGTTCCGTG
                                                58 CAAAAGACCCGCTGTCAGCACTCACTCCTCTACCTATCCAGTACAGCGACTTTGCAAAAT
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                                                                                                                                                                                                   TGTCTGGAGACGCAGGTTGCGTACATGTTACCATCGACGCGGAGCTCTACCAGTCCCTTC
                                                                                                                                                                                                                                                                                                      CCGCTCATTATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAATC
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                            Gaps
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 .6; DB 1; Length 39436; 7.8e-17;
Score 97.6; DB 1; Length 39
Pred. No. 7.8e-17;
0; Mismatches 254; Indels
           larity 51.5%;
Conservative
             1 Similarity 279; Conserv
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AF455810 15582 bp DNA linear BCT 02-JAN-2002 Xenorhabdus bovienii T228 ABC transport protein XpsD (xpsD) gene, partial cds; and peptide synthetase operon, partial sequence. AF455810.1 GI:18034620 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 11 AF455810

Xenorhabdus bovienii.

gene CDS

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PHPLYADTPVPLMVNMMEVNÖQIRCHFHYDPQVFDAELINQLIKNLITLLTAMADNQQ
QSIDSLPLMDEQEHQQVLXDPNKTDRPFPQHALIHQLFEQQABERTPDAIALSGGBKAL
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GLVPIGHPIDNTQIYILDKHDQPVPIGVIGEIYIAGAGVARGYLNKPELTAERFIRDP
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LNGKLDRKALPAPDHSAVLTREYAAPQGETEEQLADIWQKLLKIDRVGRNDNFFELGG
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                                                                                                                                                                                                                   DVSVWEFFLPLLAGTQLVMARPGGHKEALYLLEETEARGITTLHFVPSMLQSFIHLTP
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YIQALNMGHKVKIIDGKFSTTELSAGQRKRLALVAAYLEDRPLYLFDEWAADQDPVFK
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                                     1 (bases I to 15582)
Pinyon R.A. and Thomas, C.J.
Identification of a novel peptide synthetase operon in Xenorhabdus bovienii 7228
                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                 Submitted (05-DEC-2001) Microbiology and Immunology, Adelaide University, Molecular Biosciences, Victoria Drive, Adelaide, SA 5005, Australia
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988. .993
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                                                                                                                                                                    2 (bases 1 to 15582)
Pinyon, R.A. and Thomas, C.J.
Direct Submission
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/gene="peptide sy/note="putative"
1127. .441^
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  Xenorhabdus bovienii
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ORGANISM
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LONOGITVVDLPTAFWHLWAQEISAGYSWPPEQLRSVAAGGEKAEHRHLVTWLSSFGT
OKCRWLNTYGPTETTVNATSIVIDKENLCTYEDIPIGRPIANTRIYILDGRGOPVPIG
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APTLLELPTDKVRPSVQSYHGDQVTFTLSPELNSGLRALSQRHGATLFWTLLAGWGIL
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SDPFREQPHARMYRTGDLGCWRPDGTIVYLGRNDFQVKIRGFRIELGEIESQLAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGRLLTRLAEESHVLLLTQHHIISDGWSVNILMQELSTLYQAFCQDQAEPLPALTLQYA
DYALWQRQWLQGDVLEKQLDYWRSELQGAPVILELPTDKPRPTQQSYAGSRVDITLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVNTLALRIQLGDNPSVSELLARVKNHALGAYAHÖDLPFEQLVEALKPPRSLGHSPIF
QVMLALDNTPGQQYFELDGLHLHELPRTRDSAYFDLTLTLNDTEQSLVGDLEYASDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHASIERMVGYLQTILSAMVADDSLRVDDLPLLTSSQRTQLLANFNDTAIPYPKNALI
HQLFEQQVERTPDKIALVWGETQLSYSELNQRANQLAHSIMASGVHPDDRVAICAERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNGEIHISGSGVARGYLNRSELTAERFIQDPFSDIPGARMYKTGDLGRWLPDGTISYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRNDFQVKIRGFRIELGEIEAQLATCAGVKDAVVIVREDDNGDKRLVAYLIPQSGAIL
NAASLREQLSVNLADYMLPSAFVTLEAFPLNQNGKIDRPALPAPDRSASVSREYAEPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEAYAHQDLPFEQLVEVLQPPRSLSHSPIFQVMLALDNTSSKQSFELAELSLNPLALT
RNSAHFDLTLALSDTENSLTCELEYASDLFERSSIERMAGYLQNLLAAMVADDNLRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLPLLMPHERTQLLTDFNDTAVTYPQDKLLSQLFEQQVEHTPDAIALIWEDAQLSYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNQRANQLAHALIAFGVQPDDRVAICIERNLNMVIGMLGILKAGAGYVPLDPEYPAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAY ILSDSAPKLLLTQQHLQA`QLPVEKLPVWQLDDTGHLNSVAQQPTDNPDPRQLGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHHLAYIIYTSGSTGLPKGVMIEHHNVVNFTYSQCQTSELKSTDRVLQFASVSFDTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                           /PLSWAQQRLWFLTQLDPAAQTAYHMSAGLNLQGHLNQNALKAALDQIVARHEILRT
                                                                                                                                                                                                                                                                                                                                                                                                                                :VDVEGQPQQIIGSADSGFALSVQDLSPLPSTEQQAAVEECAQREALLPFDFTQGPL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALSTELKAFSQRHGITLFMTLLAGWAVLLSRISGQHDLVIGSPVANRQRHELEPLIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDMVIGFVGILKAGASYIPLDPNHPTERLAYMLSDSQPVLMLTQQHLKARLPVTNIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALDSEEHQTCIASQPKDNIDASQLGLTSQNLAYVLYTSGSTGLPKGVMIEHQNVVHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEIEQOLAAIWQNLLGLERIGRYDSFFELGGHSLLTVQVASRLRQSLNIEITLQDLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSRLSGQPDLVIGTPVANRQYSELEPLIGFFANTLALRIKLEDNPTVSALLARVKAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSDAVVVAREEGSGDKRLVAYLVPKSDVTLDAASLREQVSTHLAEYMLPSAFVILDAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CAGGTTGCGTACATGTTACCATCGACGCGAGCTCTACCAGTCCTTCGAGCCTTCTGCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ACGAACACAACACGACCTCTTTCGTCGTTCTTCTAGCTGCGTTCCGTGCCGCTCATTATC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8232 TTAATGTATTGATGAACGAACTTTCTGCGCTGTACCAAGCCTTCGGTCAGGGGCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ITGATGTCTTGCGACGCGATCTCAATCAGCTCTACTCAGCTGCGCTCAAGGACTCAAAAG
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Pred. No. 5.1e-14;
0; Mismatches 297; Indels
                                                                                                                                                                                                                                                 /product="peptide synthetase XpsB"
/protein_id="AAL57600.1"
/db_xref="G1:18034623"
                                                                     'gene="xpsB"
448. .14398
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Best Local Si
Matches 292;
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8529 AGGGCCACGTGCGACGTTGTTCATGACATTACTGGCCGGCTGGGGAATTTTGCTGTCAC 8588
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Isolation of a gene (pbsC) required for siderophore biosynthesis in
fluorescent Pseudomonas sp. strain M114
MOL. Gen. Genet. 243 (5), 515-524 (1994)
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LFVVLLASFQALLHRYSGQADIRVGVPNANRGRVEIERLIGFFVNTQVLKADIDGQMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MIEELVQLYAGFNLGHDAGLPALPIQYADYALWQRQWMEAGEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLNGLSIKPLEWQSQTAQFDLTLNTTEQAHGIEAVLKYATDLFDAATIERLAQHWNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TREVPDPENDOAGERLY RTGDLARLRCDGVIEY IGRIDHOVK INGFRIELGEIEAQLL
KHADVREAVVLAVDGISGHATGDVDCRERRTGRRRAGRTARFDQGAFARNPAGLHGSG
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                                                           420
                                                                                                                                          AACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATC 480
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                                                                                GTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGACCTG
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Direct Submission
Submitted (14-FEB-1994) C. Adams, University College Cork,
Microbiology Department, Cork, IRELAND
Location/Qualifiers
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/transl_table=11
product—blosynthetic protein C"
/protein_id="CAA54778.1"
/db_xref="G1:455514"
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/db_xref="taxon:306"
1089: .3546
/gene="pbsc"
1089: .1099
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1135, .3546
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X77699.1 GI:455513
pbsC gene, protein C
Pseudomonas sp.
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TITLE
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PSPBSC
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KEYWORDS
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Pseudomonas syringae pv. syringae syringomycin synthetase (syrE)
gene, complete cds.
AF047828
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                                                                                                              ACAGCGACTTTGCAAAATGGCAGAAGGACCAATTCATAGAGCAGGAGGAAGCAACTCAACT
                                                                                                                                         ACTACGCCTTATGGCAGCGGCAGTGGATGGAGGCCGGTGAACAGGAGCGCCAACTGGCCT
                                                                                                                                                                                                 GCCCTGCACTTCTGTCTGGAGGCGCAGGTTGCGTACATGTTACCATCGACGGCGAGCTCT
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                                                                                     Gaps
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Pseudomonas syringae pv. syringae
Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 28587)
Guenzi, E., Galli, G., Grgurina, I., Gross, D.C. and Grandi, G.
Characterization of the syringomycin synthetase gene cluster.
Link between prokaryotic and eukaryotic peptide synthetases
J. Biol. Chem. 273 (49), 32857-32863 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chiron/Vaccines, Via
                                                                                      3;
                                                     Length 3671;
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                                                                                   Indels
                                                    Score 86.2; DB 1;
Pred. No. 1.3e-13;
); Mismatches 248;
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Coation/Qualifiers

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                                                     8.68;
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                                                                    Best Local Similarity 49.7 Matches 248; Conservative
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SLRRGAEMYVALLGILKAGGAYVPIDPDLPSARQAYMLEDSSPQAVLTTRDLSDNLPA
SDLPVLVLDGHNDRAQLARQQSVNPDAKALGLQPNHLAYVLYTSGSTGTPKGVMNEHL
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GELHIGGIGVARGYLNQPQLSAERFIADPFSNDPQARLYKTGDVGRWLANGALEYLGR
NDFQVKIRGLRIEIGEIEAALAKHPAVHEAVVTAREDIPGDKRLVAYYTQSAEHTAVD
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YMVPAIYVLLEAMPLTSNGKLDRKALPAPDGDALISKGYEAPQGEIEEQIAVIMQDLL
GVEQVGRHDHFFELGGHSLLAVSLIDRLRKQDLNLNVNTVFTAPSVREMALAISQEKQ
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FTGRLADVDSPTAPFELLEVQGDGNDVEESELALSSDLCARIRTQARERGMSPAVLFH
VAWAQVLARCTGRDDVVFGTAVTGRLQGTLGAERAMGMFMNTLPVRVQLATQSVQELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGGQRVLSKAPFKLEVTDFPEVDGDTEQAIAHLRESFRQPFESV
TGQLMESRLVRCGPQLHYWFNRLHHLVADGIGAVLIAHAVSDAYSGLLEGKETLAEGP
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ATIGMFSSVSPIRVGFDPHETLVDLMNNIGTQLRRTYRHQRFPIAELNRSLRLAGNGR
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YLAQVMSDAGITLLHFVPSMLDVFLEHRSTRDFPQLRRVLCSGEALPRALQRRFEQQL
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TVAALAAAAGGGSEVVVPANLIPEHCDRITPQMLPLINLSQAQIDHVVKDMPGGVANV
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RIVFSHDPVNDRWLAMLLCHHLVSDATSLSVILQEIQAHLLGQGNALGEAVPYRNYVA
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ALRNLVDALEHTPQAALNSLSILPDDERELLLTGFNDTAHPYPRDVLIHQLIEQQAAQ
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ALLKKQPTGNPDAKALDLQPNHLAYVLYTSGSTGTPKGVMNEHLGVVNRLLWARDAYQ
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AIDVTAWECRPTDPGDSVPIGRPIANIQMHVLDALGQLQPMGVAGELHIGGIGVARGY
LNQPQLSAERFIADPFSNDPQARLYKTGDVGRWLANGALEYLGRNDFQVKIRGLRIEI
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ILFHYLLNLERDAYLVRSTIEFDSRARLDAFLEGLOTVIDRHDVLRSSVHWVGLPQAV
QVVHRQAQSPIHTLTLRPDEDALSQLDRLSDPGRLRLDLRQAPLLLAYIARDPDSERW
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ELNRQANRLAHHLIGLGIGPDDRVAICVERGVEMMYGLLGVLKAGAAYVPLDPAYPAE
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FPALLAGATLTPSREIFGSEGTENHGINPTVLHLTAAHWHTLVAEWHKOPOVAEORLO
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SGNATIGKPWANTRIYLLDAHQQPVPYGVAGEIYIGGDGVARGYLNLEEVNAERFLAD
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/note="pathovar: syringae"
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NLIGFFVNTLAIRVDLSGTPSVEALVRQVKQRTLAAQANQDLPFEQVVEVVQPQRSLS HSPIFQAMLSWQNNEDTALVLGDLTLQGVAVAGDTAKFDLALDIGEVDGQLIGTLEYA TALFDESTMRRYRGYFLRLLEAMAADDQQVLEQVPLLDTAEREYLLKDINATERTYPV GOLMHRLFEAHAEAAPQAIAVRQGEOTLTYAELDSRANALAOHLRKHGVGPGTRVAIL LDRSVELLASMLATLKCGAAYLALDRLAPEERLRFMLEDSEAIMLLSRSDLTAPDMTP RLDLDTLELSALNQEPVVPATEVAGETPACIIYTSGSTGVPKGVIVTHNGIVRLVQDN GYYDFSAEDRVAFSSNPAFDASTPEIWGALLNGCOSVITEPOVLLEPVAFAALLKRHG VTAMISSTALFNLYAGLIPEALAGLRMIMCGGERADPASFRRVREHSAQVRLFNGYGP TEGTTCATSYEIFDVLPDTLSLPIGKPNANVRVYVLDARREPVPMGVVGDIYIGGTGV ALKAALDRLVARHESLRTTFELHGEQPVQVIAAADSGFALAEDDLRSQPYEQASLNAS RIADSEAAAPFDLRQGPLIRGRLLRLADDEHMLLITQHHIISDGWSVGVLINEFTALY QAFTEQRPDPLPALSIQYADYAAWQRRTFTGERLAEQADLWREHLGGAPTLLSLPTDR ETFNOTRODYPTDLCIQHLFEAQVRTQPDAIAVAQGQRLSYADLNRQANRLAHHLIS LGIVPDDRVAICVERGVEMGILLGVLKAGAAYVPLDPAYPAERLAYMITDSQPAALL TLPGLQDRLPALSMPLVLLDDEQYQGLAECDDNPVVPTLGVRNLAYVIYTSGSTGNPK LARYMADGRIEYLGRNDFQVKVRGFRIELGEIEARLGNCKGVKEAVVIAREDNPGEKR FVAYVVAQPQTQITAAELRAELAPQLAEYMLPSAFVLLDELPLTPNRKFDRKALPAPA QLGVELGLAALFÄHPEVSALAVATÄQAGRSKFPDTVPVARDQAMPLSFGQORLMFTAQ MEGASAAYHTPAGLSLHGNLNLKALQRALERTVARHEGLRTTFMQGDDGQPVQRISPA OSNEWQQTLADAPALLMLPTDRARPALQDYAGAALPVVFDKDLTRGLKALSQRRGSTL FWTWAAAMAGLIGRLAGQDDVVIGTPVANRTRESPVGLVGLFVWTLATRYDLSDKETA ETLLARVKQQTLDADAHQDLPFEQVVEVILPPLRSLSHEPIFQAMLSWENNBASDLTLG DWTLKSIELAADTAQFDLTLDMAEVDEQLVGTLEYATALFDESTWRRYLGYFQRVLEA VVETLGAHNLAYVIYTSGSTGVPKGVMVEHRGLFAVSAAWEQLYALHAPLNHLQMAGF FDVFSADLIRSLAFGGTLVLCPRETLMDPPALYRLLSEESIGFADFVLAVLNALLGWV FMDNPFVAGERLYRSGDMARYRADGNIEFLGRNDSQAKLRGLRLELGEIEARLAEVAG VRESLVVIREDSGGTPKLIAYFVEYATRDESGPALTPRALRQQLQLNLPEYMIPAAFV DDFFALGGHSLLVMRVLAQVRQQLNLEVSPSVFFAAPVLRQFAERLGUTQDNARVAIK PVQRSGALPLSYAQQRLWFLAQLEGGSAAYHIPAGLRLRGNLDQASLQRALDRIVARH PVQYVDYALWQRDWLSGDVLQQQRQYWQQALAGAPALLT1PTDRPRPAQQDYSGQTLE LVLDTQLTRGLKALSQRHGSSLFWTVMGAWAALLGRLSGQDDVV1GTPVANRMSAEVE ALGYLNRPELTAERFSEDPFSQQAGARLYRTGDLARWLPDGNLEYLARNDGQVKVRGF RVELGETESVLHLYDGVRNSVVVAHEASPGDTRLVAYYTVHAGVAAPDPEDLRAQLSA PRPVVQSYRGGAVPVTIDAALHQRLERECQAHNVTLEMGLLSAWSVLMTRLGNERDVV IGVPSANRGRTETENLIGFFVNALALRVDLTQNPSVAQLLEQVRQTTLAAHEHQDIPF EQVIEALQPPRSMSHSPLCQVALSLDNTSIGGELKLPGLSLHPVLQAHETAQFDLMLT LASENGALNGVIEYASDLFDRSTVERFAQHFHTLLEAMVEDVAQPVLGLPLLSPAQRL ASPALLQPKAVFASGLMVHQRFEQFAAAHPQNIALVFGRHEVSYQALNRRANRLAHEL LAQGVRPDDRVAILABRGTQMICAVLAVLKSGAAYVPLDPTYPTERLGYLLTDSAPVA KLVIVPSEVARSPDDFYALVCEQQYTVLNQTPSAFRQFIQARERSPQEHALREVVFGG EALDFRSLQPWTARTPLSRTRLVNMYGITEITVHATYYPISQSEIDTAMPSLIGPALD GVMIEHRGLVNYSVDAARLFDLSQSDTVLQQNTLNFDLSVEEIFPALLAGATLAPSRE MVADDOQVLEHVALLGADEREHLLAGLNATEAPFPQDRTIHQLFEERVQAQPDAIAVA FGAORLSYAELNROANRVAHHLISLGIKPDDRVAICVERGVEMLIGVLGVLKAGAAYV PLDPAYPAERLAYMIEDSTPSALLAQRDVQAHLPTLDLPLVLLDEDQRTTLSERDDNP **EETGHDLSFMRTVVCGSDIWTAHSARQLRKLCGDHVQVVQAYGVTEASIDSTCFEFEA** NGPLVRGRLVRMANDNHVLLVTMHHILSDGWSTGVLNRELGALYAPFRQGAGDPLPAL DLAEYMVPSVFVRLDALPLTLNGKVDQKALPVPDLNAMFERTYVAPEGATEQALAEIF QELLGLERVGRHDGFFELGGHSLLAAQLVSRVRQQLNGDMALRQLFNHPTVAELAKVV DGLQTVDSDSIEPIERNAPLALSFSQQRLWFLDRLDPGASSAYHMPMSLLLRGELDHR PAPDQFATVSRDYEAPLGAIETTLAAAWQELLGVERVGRQDHFFELGGHSFLVISLIE ILRSVQDLSDDLSARIHSTARAQGVPTSVLFHAAWGLVVAATSGRDDGIFGTVLSGRS QGTSGANHALGMFINTLPMRIRLQQNSVRDIVQDAYQQLSGLLTHERAPLALAQRCSA IFGSEGTETHGIOPTVLHLTTAHWHTLVAEWHNOPQAAEQRLQHVRLINVTGDALSAQ KLKLWDEVRPAHTLLINTYGPTEATVSCTAAYVSYDAAAGSEGSGNATIGKPMANTRI YLLDAHQQPVPYGVAGEIYIGGDGVARGYLNLEEVNAERFLADPFSESPDARMYKTGD DDAFASREHVEPQGATEIALAQIWQSLLDLERVGRHDQFFELGGHSLLAMRLISQARH DTGFNLOMHDLOGLADAEEKLOALASEESLOSFDLOOGPLIRGRLIRMAEDHHVLLLT LHHIVSDGWSVDVLTRELSALYAAFSQDQDDPLAPLELQYLDYAVWQRRWLSGDVLQQ TSQVDGVLPIGRALANTRIYLLDELGQAVPPGVAGELYIGGAGIARGYLNLPQLTAER RMAALPLSANGKLDRRALPEPDADAFDQHDFEAADGPLETAIAAIWADVLGVAQVGRH EALRTTFVQEQGQPAEQRISAAETGFRLQLQVLAGQTDAEDKLLAIAAQEASEHFDLV LLAQSACLDVLPAHSVPVLTLGADNDSADLADESVDRNPEPAALGLSREHLAYVIYTS GSTGLPKGVLVEHGNVARLFDATAGQFNFGHEDVWTPFHSFAFDFSVWEIWGALCYGG DLCLRILDDYQQPVPVGVNGEIYIGGAGVARHYLNRTELNAERFIADPYALQSGARLY RTGDVAHYRSDGGVVNVGRNDSQIKIRGFRIELGEIEAQLLACPEVREAMVILREDRP GDKRLVAYLIAEDGAAPESALLRSQLASVLAEHMLPSAFVTLETWPLTTNGKLDRAAL RLRQIGLLLDVSTVFSAPTLQAMAAVLAGGTAAERVAPANLIPVDCTALTPDMLPLVK LTRQELEHIVADVPGGVANVQDIYPLSSLQEGILFHHLLQSEGDAYLMRTLATFDSRA LLDKFLGALQVVINRHDIMRSSLRWQGLPQPVQVVHRQAQLPVIQLDTAPGEDALOML RERTNTYHMRLDLQQAPLIAAYITYDTRQEKWLMALLDHHLISDNVTLRLIMGEIQAV MDGRADALPPSQPYRNFIARAACVSQAEHEAYFRQLLGDVDTTTAPYGVLDVRGGDAT

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FNDTASDFAPAVPIHALFEDQVRRNPDAVALVYEDRQLSYRQLNRRANHVARQLLQLG
VQPDERVAICAERSLDMIAGLLGVLKSGAAYVPIDPAHPADRWAFWLQDSQPRALLTQ
                                            GALSLPVGDTPLMLLDSAESLLAADDQAFDANPVVDGLTAENLAYVIYTSGSTGQSKG
VMVEHRSVFNFWNVLTRTTHQHCPTPATVALNAGFFFDMSIKGISQLFSGHKLVIIPQ
LLRANGSELLDFLEAHQVHAFDSTPSQLDTLLSAGLLERSSYQPVSVLLGGEAINAST
                                                                                                                                                             EYMGRNDFQVKVRGFRIELGEIENVLLAVPGIREVVVIARNDSQGDSDSQRLVAYVCG
ESVAAEHLRSELLRHLPEYMVPSAFVQLDALPLTANGKLDRRALPAPGQDALASKVYE
                                                                                                                                                                                                                               LEDAPTVRGLASLVNRAAAPGEAQSTPRANRSCRLPLSFSQQRUWFLDHLDHAAGAAYH
LPMALRLTGALDTAALEATLDRLVARHETLRTRFELVDGEPVQKTAPADSRLPLLKQD
LRDLSGDERTSTLARLGQENÄTQLFDLTKGPMLRGHLLRVADAEHVLLITLHHIVSDG
                                                                                                                                                                                                                                                                                                         WSNSVLAQEVSALYAAFSQCQKDPLPALPLQYVDYAAWQRQSLDGPALQAQIDFWRKH
LEGAPSVLNLPLDRPRPAIQSYTGGMVEHVFSPALSADLRAFSQAQGSTPFWVLLAGW
SMLMSHLSEQTDVVVGTPVANRQHPELEPMIGFFANTLALRVATDRETRLNDMLDRIK
                                                                                                                                                                                                                                                                                                                                                                            SLTLAAYNHODLPFEQVVSALOPTRNVSHSPLFQVMLSLDNTPPSLLQLPDLEVELLD
SEHHTTQFDLSLSLVDSSESLGGGLQYSSDLFDKTTAQAIMQLFARVLENMVSDARQS
IGQVLDNTPALPRSAHTATIAATVEDEQPEALPYEAPEGETEIALANLWKELLKLEKV
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LEQQAPEALSEGQFLMDWLPEQLDPEVFRQLTELAGTDAIDEMLALCWAHRLLPEELP
QDVDATLLRSHLAVAHATHIAIGNYVSPPAPLTVTLFTASAEERDDPLLGWTALLDSP
                                                                                                                 WEKLRNCPTIRLYNMYGPTECTVDATIDLIRDLGEKPSIGRPIANVQVHVLDARGEPA
                                                                                                                                            PLGVAGEIHIGGSGVARGYLNRDELSAERFIVDPFSDAANARLYKTGDLGRWLADGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGTTTTTTTGTCAACGCCCTGGCCCTGCGGTTGATCTGACGCAGAACCCGAGCGTGGC
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8997 c 8675 g 5494 t
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Polyangium cellulosum
Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
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llarity 51.3%; Pred. No. 1.8e-13;
Conservative 0; Mismatches 190;
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AX024319
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Search completed: June 4, 2003, 20:51:10
Job time : 2769 secs
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                                                                                                                                                                                                                                                                                                                                         175 TCAAAGACTCTTCC---CCAGCAAAGATCCCGACCGACTTTGCCCGCCCTGCACTTCTGT
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Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
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                                                                                                                                                            Score 85.6; DB 1; I
Pred. No. 2.4e-13;
0; Mismatches 259;
                                                                       1. .37856
/organism="Polyangium cellulosum"
/db_xref="taxon:56"
a 13666 c 12913 g 5622 t
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Patent: DE 19846493-A 1 13-APR-2000;
BIOTECHNOLOG FORSCHUNG GMBH (DE)
Location/Qualifiers
1 (bases 1 to 37856)
Beyer, S. and Mueller, R. J.
Patent: DE 19846493-A 13-APR-2000;
BIOTECHNOLOG FORSCHUNG GMBH (DE)
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Sequence 1 from Patent DE19846493.
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al Similarity 50.2%;
270; Conservative
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                                                                                                                                     61 AAGACCCGCTGTCAGCACTCCTCTACCTATCCAGTACAGCGACTTTGCAAAATGGC
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                               6
 Length 37856
                               Indels
                             0; Mismatches 259;
Score 85.6; DB 6;
Pred. No. 2.4e-13;
8.6%;
                           270; Conservative
             Best Local Similarity
Matches 270; Conserv
                                                                                                                  121
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us-09-482-788-1\_copy\_4000\_5000.rng

	Gencore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
OM nucleic - nucle	OM nucleic - nucleic search, using sw model
Run on: Ju	June 4, 2003, 17:28:42 ; Search time 271.5 Seconds (without alignments) 8302.948 Million cell updates/sec
Title: US Perfect score: 10 Sequence: 1	US-09-482-788-1_COPX_4000_5000 1001 1 caattgatgtcttgcgacgccccaagtctctgcttacccc 1001
Scoring table: ID	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 21	2185239 seqs, 1125999159 residues
Total number of hi	Total number of hits satisfying chosen parameters: 4370478
Minimum DB seq length: 0 Maximum DB seq length: 200000000	jth: 0 jth: 2000000000
Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45	Minimum Match 0% Maximum Match 100% Listing first 45 summaries

# Database : N\_Geneseq\_101002:\*

N_Geneseq_101002:*	1: /SIDS2/gcgdata/geneseg/genesegn-emb1/NA1980.DAT:*	2: /SIDS2/gcgdata/geneseq/genesegn-emb1/NA1981.DAT:*	3: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1982.DAT:*	4: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1983.DAT:*	5: /SIDS2/gcgdata/geneseg/genesegn-emb1/NA1984.DAT:*	6: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1985.DAT:*	IDS2/	8: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1987.DAT:*	9: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1988.DAT:*	<pre>10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*</pre>	`	<pre>12: /SIDS2/gcgdata/geneseq/genesegn-embl/NA1991.DAT:*</pre>	<pre>13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*</pre>	<pre>14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*</pre>	<pre>15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*</pre>	<pre>16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*</pre>	: /SIDS2/	` 	<pre>19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*</pre>	<pre>20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*</pre>	21: /SIDS2/gcgdata/geneseq/genesegn-embl/NA2000.DAT:*	22: /SIDS2/gcgdata/geneseg/genesegn-embl/NA2001A.DAT:	23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:	24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- •	7	8	3	4	2	9	7	8	6	Ä	H	1:	H	7,	ä	1(	H	ã	19	7	5	5.	5	2,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

•	Description	encoding a cvc	elia sterilia c	niveum Cyclospo	niveum alanine-	T. niveum alanine-	cellulosum DNA	Pseudomonas aerugi	rum sensing con	Nucleotide sequenc
	Desc	DNA	Myc		T. T.	H	. S.	Pse	ono	Nuc
	ID	AAA58762	AAF79702	AAQ54386	AAQ78276	AAQ78281	AAA11992	AAS51470	AAF81367	AAA58472
	DB	21	22	15	15	15	21	23	22	21
	Match Length DB ID	11212		-						
Query	Match	100.0	39.5	33.9	16.8	16.8	8.6	7.6	7.5	7.4
	Score	1001	392	339.4	168.6	168.6	85.6	75.6	75.4	74.2
Result	NO.	1	7	m	Ċ T	c S	9	7	œ	6

	10	71.8	7.2		24	ABK74876	Bacillus lichenifo
	11	70.4	7.0		22	AAF26319	Pseudomonas sp lip
	12	67.4	6.7		21	AAA14651	Nucleotide segment
	13	65.8	9.9		24	AAL40781	88421nt genomic DN
	14	64.2	6.4		22	AA166165	Bacillus subtilis
	15	62.8	6.3			AAQ54388	T. qeodes Cyclospo
	16	60.4	0.9			AAS54136	Pseudomonas aerugi
D		60.4	6.0	4		AAI99683	Mycobacterium tube
O		60.4	6.0	4411529	22	AAI99682	Mycobacterium tube
	19	59.8	6.0		12	AAQ10190	Cephalosporin anti
	20	56	5.6		24	ABK74880	Bacillus lichenifo
O		52.4	5.2		22	AAF26318	Pseudomonas sp lip
	22	52.4	5.2		14	AAQ40706	Bacillus subtilis
	23	51.8	5.2		22	AAF90035	Nucleotide sequenc
	24	51.8	5.2		22	AAF90033	Nucleotide sequenc
O		51.8	5.2		22	AAF90032	
	26	48.6	4.9		21	AAA58471	Nucleotide sequenc
	27	48.4	4.8		22	AAF81368	Quorum sensing con
	28	47.2	4.7		24	ABK74875	Bacillus lichenifo
	29	47.2	4.7		24	ABK74878	Bacillus lichenifo
	30	47.2	4.7	4	22	AA199683	Mycobacterium tube
	31	47.2	4.7	4411529	22	AAI99682	Mycobacterium tube
	32	46.2	4.6			ABA89199	Escherichia coli p
U		46.2	4.6			ABA89188	Escherichia coli p
	34	41.2	4.1			AAQ13608	ACV synthetase gen
	35	41.2	4.1			AAQ48231	Vector containing
	36	39.8	4.0			AAF90034	Nucleotide sequenc
	37	38.6	3.9	7178	21	AAA59145	DNA. encoding a pep
υ		36.8	3.7		20	AAZ01425	Complete genome se
O		36.2	3.6	273254	21	AAC81914	Chlamydia pneumoni
	40	36.2	3.6	1230025	20	AAX91990	Nucleotide sequenc
	41	35	3.5	4590	22	AAH24065	Yeast AOD9604-asso
O		4	3,5	3519		AAS81987	DNA encoding novel
O		34.8	3.5	35	23	ABL20034	Drosophila melanog
O		4	3.5	390	23	ABL18792	Drosophila melanoq
	45	4	3.5	4024	20	AAX84595	MTG16b protein cod
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4720 ACATGGAGTTCCATCTGTTTCAAGAAACCGACAGCCTTAAAGGTAGCGTCAACTTTGCCG 4779
                                                                                                                                                                                             The present sequence encodes a cyclic depsipeptide synthase from Mycelia sterilia. The protein encoded by this sequence, or a protein containing an addition, deletion and/or substitution of one or more amino acid residues is useful for the efficient production of the anthelmintic PF1022 (cyclo(D-lactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-methylleucyl-D-3-phenyllactyl-L-N-
                                                    4780 ATGAGCTGTTCAAAATGGAGACTGTTGAAAATGTCGTCAGAGTATTCTTTGAGATTCTG
                                                                                                                        ATGAGCTGTTCAAAATGGAGACTGTTGAAAATGTCGTCAGAGTATTCTTTGAGATTCTGA
                                                                                                      841 GAAACGGGCTTCAAAGTTCGCGGACACCAGTCTCAATACTTCCTTTGACTGATGGCATTG
                                                                                                                                                                           TGACTCTTGAAAAATTGGATGTTCTCAACGTCAAACATGTCGACTATCCCCGAGAATCGA
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PF1022; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanai K,
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63.3%; Pred. No. 3.4e-116;
iive 0; Mismatches 360;
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I, Murakami
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Futamura T, Kleinkauf.
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06-APR-2000; 2000JP-0104291.
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637; Conservative
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P-PSDB; AAB73958.
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Aihara S,
                                    781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CAGGTTGCGTACATGTTACCATCGACGCGAGCTCTACCAGTCCCTTCGAGCCTTCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing a heterologous polypeptide for production of antibiotics comprises cultivating a mutant of a parent filamentous fungal cell comprising a nucleic acid sequence encoding cyclohexadepsipeptide
                                                                                                                                                                           Q
                                                                                                                                                   The present sequence encodes a cyclohexadepsipeptide synthetase polypeptide. The specification describes a method for producing heterologous polypeptide. The method comprises cultivating a mutant of a parent filamentous fungal cell, which produces less cyclohexadepsipeptide than the parent filamentous fungal cell which produces less cyclohexadepsipeptide than the parent filamentous fungal cell wh production of biologically active compounds e.g. antibiotics.
                                                                                                                                                                                                                                                                                                                             100.0%; Score 1001; DB 21; Length 11212; 100.0%; Pred. No. 2.2e-314; Ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                           Sequence 11212 BP; 2808 A; 2844 C; 2658 G; 2901 T; 1 other;
                                                                                                                     55; Fig 1A-I; 76pp; English
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 1001; Conservative
2000-482833/42
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/\*tag= d
/note= "SalI restriction fragment,
fragment, Claim 5"

/note= "SalI restriction fragment, fragment, Claim 4" 37781..40244

/\_rag= a /product= Cyclosporin synthetase 40239..43129 /\_rtag= b

Location/Qualifiers 885..46730

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yme; cyclosporin; synthetase-like activity; Tolypocladium niveum;
inflatum GAMS; biosynthesis; vector; cyclosporin synthetase; ss.
                                                                                                                                                                                                                                                                                                                                         SANDOZ PATENT GMBH.
SANDOZ-ERFINDUNGEN VERW GES MBH.
         niveum Cyclosporin synthetase gene
                                                                                                                                                                                                                                                                                                                                                                         Schneider E,
                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated DNA sequence - synthetase like activity
                                                           Polypocladium niveum
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-010432/02.
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(SANO ) SANDOZ
                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated DNA
                                                                                                                       misc_feature
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29-APR-1993;
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                          -TGATCCTCTATCGGTGGTGAGCCCACTCCCACTCCACTACCGCGACTTTCCGTTTGGC
                                                                                                                                          GACCTGAACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAATCAACA
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                                              GAGACGCAGGTTGCGTACATGTTACCATCGACGCCGAGCTCTACCAGTCCCTTCGAGCCT
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      AAGACCCGCTGTCAGCACTCCTCTACCTATCCAGTACAGCGACTTTGCAAAATGGC
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93AT-0000437. 93CH-0001310. 93CH-0001375.

LTD.

93EP-0810474 92AT-0001403

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ACCCGCTGTCAGCACTCACTCCTCTACCTATCCAGTACAGCGACTTTGCAAAATGGCAGA 123
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                                                            like activity. This sequence was isolated from Tolypocladium niveum (formerly known as T. inflatum GAMS). The enzyme encoded by this sequence catalyses the peptide biosynthesis of cyclosporins and structurally related molecules. This sequence may be used for the production of cyclosporin by transforming a vector containing this sequence in to a recombinant host. This allows effective production
                                           sequence encodes an enzyme which has cyclosporin synthetase
                                                                                                                                                                                                                                                                                          Length 46899;
                                                                                                                                                                                                                                              Sequence 46899 BP; 10651 A; 13513 C; 12509 G; 10226 T; 0 other;
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                                                                                                                                                                                                                                                                                                               1.1e-98;
hes 391;
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Pred. No. 1.1e-
0; Mismatches
Claim 6; Page 17-41; 93pp; English.
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ilarity 60.1%;
Conservative
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Best Local Similarity
Matches 603; Conserv
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BP 46899

DNA;

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RESULT 3

AAQ54386

(first entry)

08-JUL-1994

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-----AGGACCAATTCATAGAGCAGGAGAACTCAACTACTGGAAGAAGCAACTCA 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ITGATGTCTTGCGACGCGATCTCAATCAGCTCTACTCAGCTGCGCTCAAGGACTCAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 ACCAGGACGAGGAGGTCGCTGAGCAGGAAAGGCAGCTCGGATACTGGATCGAGCAGCTCG
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                                                                                                                                                                                                                                  New nucleic acid encoding eukaryotic alanine racemase - and related vectors, host cells and recombinant enzyme, useful for producing cyclosporin derive. or increasing cyclosporin producing also new glyceraldehyde-3-phosphate dehydrogenase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 3973;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3973 BP; 917 A; 1036 C; 1103 G; 917 T; 0 other;
                                                                                                                                                                       Schoergendorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 254;
                                                                                                                                                                                                                                                                                                                                                                                                                              16.8%; Score 168.6; DB 1
56.4%; Pred. No. 1.2e-43;
                                                                                                                                              (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH
                                                                                                                                                                       HP, Schneider-scherzer E,
                                                                                                                                                                                                                                                                                                Disclosure; Fig.5; 82pp; German.
                                                                 93DE-4312856.
93DE-4314610.
93DE-4316419.
                                          94WO-EP01272
                                                                                                                    LTD.
PATENT GMBH.
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nes 337; Conserv
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(SANO ) SANDOZ
                                        23-APR-1994;
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                10-NOV-1994
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AAQ78276/c
Th AAQ78276 standard; DNA; 3973
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                                                                                                                                                                   238 ACGCAGGTTGCGTACATGTTACCATCGACGGCGAGCTCTACCAGTCCCTTCGAGCCTTCT 297
                                                                                                                                                                                                                                                    GCAACGAACACAACACCACCTCTTTCGTCGTTCTTCTAGCTGCGTTCCGTGCCGCTCATT 357
                                                                                                                                                                                                                                                                                                                                       358 ATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGAC 417
                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAG 477
  -----AGGACCAATTCATAGAGCAGGAGGAACTCAACTACTGGAAGAAGCAACTCA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 ACGAGGACGACACCTTCGAGTCGGTGCTGCGGCAGATCATGTCCGTCATGACAGAGGCAC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rolyketide biosynthesis; heteropolyketide biosynthesis; mutasynthesis; epothilone; cytotoxic; immunosuppressant; antibiotic; antifungal; plant-protection; ds.
                                                                                                                                                                                             AAACTGGCAAGATCTCCTTCCAGATGGATCGGTACACAAAGAAGAACTCCTGGCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         538 TCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTGGATCCA 594
                                                                                  /note= "AGT start codon given in the specification" 9855. 11393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCCAACGCGGACGTCCCCTTTGAGCGCATCGTGTTTGTGCTGCCGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellulosum DNA encoding polyketide and hereropolyketide enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "ORF5-3-oxoacyl-ACP-reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "ORF6-polyketide synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "ORF3-aminotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product= "ORF1-tRNA synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "ORF2-monooxygenase"
complement (8433..9550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "gtg start codon"
complement (6374..7111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "GTG start codon"
2212..13658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
complement (3398.6100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "ACC start codon
15374..19984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA11992 standard; DNA; 37856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "O]
20003..27889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A genomic DNA library of T. niveum ATCC 34921 was screened with probes based on the isolated alanine-racemase (AR) enzyme. Lambda clone RAC4 contained a 1.1 kb PstI fragment, a 1.9 kb ExoRi-rsall fragment and a 650 HindIII-PstI fragment, which were subcloned in plasmid vectors and combined to give the sequence of the AR DNA (see also AAQ78276).
538 ¡CGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTGGATCCA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ITGATGICTIGGGACGCGATCTCAATCAGCTCTACTCAGCTGCGCTCAAGGACTCAAAAG
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                     ATGCCAACGGGAGGTCCCTTTGAGCGCATCGTGTTGCTGCCGGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.8%; Score 168.6; DB 15; Length 3973; 56.4%; Pred. No. 1.2e-43; ive 0; Mismatches 254; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding eukaryotic alanine racemase - and related vectors, host cells and recombinant enzyme, useful for producing cyclosporin derivs. or increasing cyclosporin produ. also new glyceraldehyde-3-phosphate dehydrogenase gene.
                                                                                                                                                                                                                                                                                                                   Alanine-racemase; glyceraldehyde-3-phosphate-dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3973 BP; 917 A; 1035 C; 1104 G; 917 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schneider-Scherzer E, Schoergendorfer K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SANO ) SANDOZ LTD.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1953.3180
/*tag= a
2035.2110
/*tag= b
                                                                                                                                                                                                                                                                                                                                       cyclosporin; immunosuppressive; ss.
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                                                                                                                            AAQ78281/c
ID AAQ78281 standard; DNA; 3973 BP.
                                                                                                                                                                                                                                                                                                                                                                              Folypocladium niveum ATCC 34921
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93DE-4314610.
93DE-4316419.
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                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                       I. niveum alanine-racemase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 56.4 nes 337; Conservative
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P-PSDB; AAR65964.
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04-MAY-1993;
17-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HP,
                                                                                                                                                                                                                                06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                            532 CAGCATTCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTGG 589
                                                                                  20715 CGTTCCGGGGCTCCCAGCGCGTTCCGACTCCCACTCTCCCTGCAACAGGCGGTGCAGG
                                                                                                                               292 CCTTCTGCAACGAACACAACACGACCTCTTTCGTCGTTCTTCTAGCTGCGTGCCG
                                                                                                                                                                                                                             412 ACCGACCTGAACTGGAGGATATCATCGCTGTTGTCAATACGCAGTGTATGCGAATCA
                                                       232 CTGGAGACGCAGGTTGCGTACATGTTACCATCGACGCGGGGGCTCTACCAGTCCCTTTCGAG
                                                                                                                                                                20775 CGCTCAGCCGGCAGGAAGGCGCGACCCCTTCATGACGCTGCTGACGCGTTCAGCGTGC
                                                                                                                                                                                                      352 CTCATTATCGTCTCACAGCTGTTGAÄGACGCTGTCATTGGTACACCAATTGCGAATCGCA
                                                                                                                                                                                                                                                                                                                                                 472 ACATAGATCATCACGATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa DNA for cellular proliferation protein #55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Seq ID No 4052; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-253625P.
2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAU33611
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22-DEC-2000;
16-FEB-2001;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAGACCCGCTGTCAGCACTCACTCCTCTACCTATCCAGTACAGCGACTTTGCAAAATGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        products effect or are involved in the enzymatic biosynthesis. In managynthesis or partial synthesis of polyketide or heteropolyketide compounds (II). (I) can be inserted into an expression vector and to transform or transfect prokaryotic or eukaryotic cells with the aim of obtaining strains that produce large amounts of polyketide or heteropolyketide compounds, especially epothilones, which have cytotoxic and/or immunosuppressant and antibiotic and antifungal activities and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are useful as plant-protection agents. This sequence represents the DNA sequence isolated from Sorangium cellulosum which is described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAAAGACTCTTCC---CCAGCAAAGATCCCGACCGACTTTGCCCGCCCTGCACTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes a novel DNA sequence (I) whose expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence coding for products involved in the biosynthesis of polyketide or heteropolyketide compounds, especially epothilone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
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                                                                                                                                                                                           product= "ORF10_transcription regulator"
33128.33613
'*tag= k
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "ORF14-transcription regulator"
/note= "GTG start codon"
                                                                                                                                                                                                                                                                                                                                                                                    /product= "ORF13-transcription regulator"
complement (35730 .36242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                      :t= "ORF11-regulation element"
"GTG start codon"
                                                                                                                                                                                                                                                                                                                              /product= "ORF12-regulation element"
complement (35255.,35616)
                 "ORF7-peptide synthetase"
                                                                                                                          product= "ORF9-regulation element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.6e-16;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                    /product= "ORF8-transpeptidase"
complement (30040..31720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.6%; Score 85.6; 50.2%; Pred. No. 4.
                                                                                                                                                 stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 20-33; 36pp; German.
                                                                                                                                                                                                                                                                           note= "GTG :
3661..34077
                                    8251..29400
                                                                                                                                                                1982..32932
                                                                                                                                               "cgc
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/product= "
                                                                                                                                                                                                                                                          product-
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                                                       ′*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                            *taq=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mueller R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-294101/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE19846493-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                      Quorum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGCGAAGGCTGATCGGCGCCTTCCTCAATACCCAGGTGCTGCTGCCGGCTCGACG 6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1846 GCGACCTCTACCGCTTCGACCTGAGCCCCGAGCTGCCGAGCGCGTGCGCGCTTCAACG 5905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAGATGAGCGTCGGCGAGCTGCTTGAGCAGGTGCGGCAGACCGTGATCGATGGCCAGT 6145
                                                                                                                                                                                                                                                                                                                                                                                                                                          CGATGGACATCTTCGCCCGCGAACTGGGCGCGCTCTACGAGGCCTTCCTCGACGACCGCG 5665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480
                                                                                                                                    programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGTTGCGTACATGTTACCATCGACGGCGAGCTCTACCAGTCCCTTCGAGCCTTCTGCA 300
              Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella phoemoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTGGAGGGGGGGGGCGCAGCCCAGCTACTAGGAAGGCCCAGCTGGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTACAGCGGCCAGCAGGACGTGCGTATCGGCGCGGTGGCGGAACCGCATCCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 AACTGGAGGATATCATCGCCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGAACACAACACGACCTCTTTCGTCGTCTTCTAGCTGCGTTCCGTGCCGCTCATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5906 CCGCCCGCGGGCTGACCATGTTCATGACCATGACCGCCACCCTTGCGGCCTTGCTCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 ATCACGATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACAGCAGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                         1 CAATTGATGTCTTGCGACGCGATCTCAATCAGCTCTACTCAGCTGCGCTCAAGGACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGACCCGCTGTCAGCACTCACTCCTCTATCCAGTACAGCGACTTTGCAAAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCGCCGCTGGAGCCGTTGCCGGTCCAGTACCTGGACTACAGCGTGTGGCCAGCGCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The prokaryotes used are
                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                     Length 13029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCACCAGGACCTGCCGTTCGACCACCTGGTGGAAGCCCTGCAGCC 6191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 AGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCC 586
                                                                                                                                                                                                                                                                                                  Sequence 13029 BP; 1978 A; 4677 C; 4485 G; 1889 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                  7.6%; Score 75.6; DB 23; llarity 45.6%; Pred. No. 4.5e-13; Conservative 0; Mismatches 319;
themselves and the encoded proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quorum sensing controlled gene gsc109 ORF.
                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 267; Conserv
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Matches
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in a cell density dependent fashion. This "bacterial signalling" is called "quorum sensing and response". Quorum sensing allows a bacterial species to sense its own number and requiste gene expression according to population density. The present sequence is an open reading frame (OFF) of a Pseudomonas aeruginosa quorum sensing controlled gene. Inhibitors of quorum sensing signalling renders a bacterial population more susceptible to treatment. The present invention relates to a method for identifying modulators of quorum sensing signalling in Pseudomonas aeruginosa bacteria. Modulators of quorum signalling may be used to treat P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGACCCGCTGTCAGCACTCACTCCTCTACCTATCCAGTACAGCGACTTTGCAAAATGGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to coordinate expression of specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aeruginosa infections. P. aeruginosa is an opportunistic pathogen of immunocompromised individuals (burn patients, cystic fibrosis patients, patients undergoing immunosuppressive therapy and patients with AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAATTGATGTCTTGCGACGCGATCTCAATCAGCTCTACTCAGCTGCGCTCAAGGACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGGACAGCGGCGCGCGCGCGCAGCTGGATTACTGGCGTGAGCGCCTGGGCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
.erial; bacterial signalling;
immunocompromised; burn; cystlc fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7335 BP; 1184 A; 2256 C; 2625 G; 1270 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signaling in E
infections in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75.4; DB 22
Pred. No. 3.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying modulators of quorum sensing aeruginosa bacteria, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 46; Page 108-110; 115pp; English.
                                                  immunosuppressive therapy; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria signal to one another
  antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%;
Similarity 43.7%;
                                                                                                                                                                                                                                                                                   2000WO-US24141
                                                                                                                                                                                                                                                                                                                                            99US-0153022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunocompromized patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433; Conservative
                    pathogen;
                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                     (IOWA ) UNIV IOWA RES
(QUOR-) QUORUM SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-265973/27
  sensing;
                                                                                                                                                                    WO200118248-A2
                             opportunistic
                                                                                                                                                                                                                                                                                   01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                            03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                      838
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                                                                                                                                                                                                                                                                                                                                                                                                                      839 GAGAAACGGGCTTCAAAGTTCGCGGACACCAGTCTCAATACTTCCTTTGACTGATGGCAT 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                 879 GCGCGGCATGCTGGAAAACCCGCAGGCCAGCGTCGACTCGCTGCCGATGCTCGATGCCGA 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            899 IGTGACTCTTGAAAATTGGATGTTCTCAACGTCAAACATGTCGACTATCCCCGAGAATC 958
                                                                                                                                                                        584 CGCACCAGGATCTGCCGTTCGAGCAATTGGTCGATGCCTTGCAGCCCGAACGCA----A
661 GATTCAAGTTCCAGGGTCTCGAGTCCGTACCTGTGCCTAGCA--AAGCGTACACTCGATT
                                                                                                                                                                                                                                                                                 699 recceaagregargerracacaregasagrirracerasgargerecescacarr
                                       AACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATC
                                                                 AGGTCGAGCGCCTGATCGGCTTCTTCGTCAATACCCAGGTGCTGCGTTGCCAGGTCGATG
                                                                                            ATCACGATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACAGCATTCG
                                                                                                                       541 AGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGGCCTGGATCCAGAGATC
                                                                                                                                                                                                      TGTCAAGCACACTCTCGCACAACTCATTTTGCAGTGCACTCACAGAAGGACCTTGGAA
                                                                                                                                                                                                                                                                                                               719 TGACATGGAGTTCCATCTGTTTCAAGAAACCGACAGCCTTAAAGGTAGCGTCAACTTTGC
                                                                                                                                                                                                                                                                                                                                 779 CGATGAGCTGTTCAAAATGGAGACTGTTGAAAATGTCGTCAGAGTATTCTTTGAGATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_except= (pos: 1..3, aa: Met)
/note= "ORF31; encodes AAB07580"
925..9450
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/note= "ORF32; encodes AAB07581"
9447..10802
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1..354
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642 CCGGGCTCCCTCCGCTCGACGTCCAGTACGCCGACTTCGCCGTCTGGCAGCGGTCCTGGA 5701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 CAGCACTCACTCCTACCTATCCAGTACAGCGACTTTGCAAAATGGCAGAAGGACCAAT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 T----CATAGAGCAGGAGAAGCAACTCAACTACTGGAAGAAGCAACTCAAAGACTCTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing open reading frames (ORRS) 31.40. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB07583, AAB07584, AAB07585,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules
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"ORF37; encodes AAB07586"
                                                                                                                                                                                                                                                                        _except= (pos: 1..3, aa: Met)
"ORF39; encodes AAB07588"
                                                                                                                                                                                                                                                                                                                                         /note= "ORF40; encodes AAB07589"
/note= "no termination codon given"
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Pred. No. 1.6e-12;
0; Mismatches 258;
                                     encodes AAB07584"
                                                                                         encodes AAB07585'
                                                                                                                                                                                                                 encodes AAB07587"
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AAB07586, AAB07587, AAB07588, AAB07589
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                                 "ORF35;
                                                                                                                                                                                                               "ORF38;
                                                                                        "ORF36;
                                                                                        /note= "ORF36
13928..14746
                                                                                                                                                                                                                                                                                         'note= "ORF39
.7646..18659
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ilarity 49.1%;
Conservative
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05-FEB-1999; 99US-0118848.
05-JAN-2000; 2000US-0477962.
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/note=
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Les 258; Conserv
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genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring genes in one or more second Bacillus cells. The method is useful for monitoring genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array available. This sequence represents a genomic sequence information is the method of the invention.
                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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nes 145; Conservative
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                                                                                                                                                                                                    Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                 424 TGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATCATC
                                                                                                                                                                                                                                                         3822 AGACCGTCGAGTTCCCCCTGCCCGCACTGGTCGCGCGGGCTGGAAGCGCTTCTGCCGGG
                                                                                                                               AACACAACACGACCTCTTTCGTCGTCTTCTTCTAGCTGCGTTCCGTGCCGCTCATTATCGTC
                                                                                                                                                                                     364 TCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGACCTGAAC
                                                                       244 GTTGCGTACATGTTACCATCGACGCGAGCTCTACCAGTCCCTTCGAGCCTTCTGCAACG
                                                                                                                                                                                                                                                                                                                                                                        ACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCCTG 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK74876 standard; DNA; 3471 BP.
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27-MAR-2001; 2001US-279526P.
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0
                                                                                                                            Length 3471;
                                                              Sequence 3471 BP; 883 A; 794 C; 995 G; 799 T; 0 other;
                                                                                                                            DB 24;
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                                                                                                                         Score 71.8; DB 24
Pred. No. 3.6e-12;
                                                                                                                                                                                       0; Mismatches
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1354 GAAATCAGCCTGCAGGCCCAGGCCAACAAGGACCTGCCATTCGACGCTCTGGTCGAGGCG 1413
                         GCTACGACGACAGCATTCGAGAACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces hygroscopicus var ascomyceticus; immunophilin; fr.506 binding protein; polyketide compound; transplant rejection; graft-versus-host disease; uveltis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple scleroders; primary biliary cirrhosts; scleroderma; neurite outgrowth; nerve regrowth; parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
                                                                                                                                                                                                                                                                                                                                                                                                              FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                      Nucleotide seguence of the FK-520 biosynthetic gene cluster.
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complement (10987..11247)
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complement (11244..12092)
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complement (13212..23988)
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/note= "fkbc gene"
complement (13452..13662)
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complement (12113..13150)
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/note= "fkbR2 gene"
complement (4595..5488)
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complement (412..1836)
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/note= "fkbW gene"
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/note= "fkbV gene"
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note= "fkbE gene"
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'note= "fkbF gene"
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'note= "fkbG qene"
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                                                                                                                                                                                                                                                                                                                                        having the biological function of Theopeptide Synthase. The invention also describes (1) recombinant expression vectors containing (1): (2) prokaryotic and eukaryotic cells transformed our transfected with (1) or the vector of (2): (3) production of lipopeptide synthases by culturing cells of (2): (4) expression products (II) of (I), and synthetic proteins or peptides with the same sequences; (5) mono- or poly-clonal antibodies (Ab) specific for (II): (6) hybridoma cells that produce monoclonal Ab; cragments, are useful for expression of recombinant lipopeptide synthases, and as probes and primers for detection, isolation and synthases, and as probes and primers for detection, isolation and complification of full-length cDNA sequences. (I) are used to produce transgenic plants. Lipopeptide synthases are useful for production of antiviral, antibacterial or antifugal lipopeptides, particularly useful for treatment of plants, and for production of lipopeptide surfactants used for increasing bloavallability in microbilal depolution processes (acting as menisifiers) and in tertiary crude oil recovery. Individual subunits from different lipopeptide synthases may be combined to allow subunits from different lipopeptide synthases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1174 TCGTTCGGCCTGCTGGCGCCGCTACAGCGGCAACGAGAAGATCAACATCGGCGTGCCC 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGTTCCGTGCCGCTCATTATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCA 398
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                                                                                                                                                                                                                                                                                                                         This invention describes a novel DNA sequence (I) that expresses products
                                                                                                                                                                               New DNA encoding a bacterial lipopeptide synthase, useful e.g. for producing antimicrobial agents, surfactants with increased bioavailability in microbial depollution methods, and transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGCACTTCTGTCTGGAGACGCAGGTTGCGTACATGTTACCATCGACGGCGAGCTCTAC
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                                                                                  Hilbert H;
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                                                                                Hoheisel J, Duesterhoeft A, aetz M, Heim S, Golyshin P;
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); Mismatches 276;
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BIOTECHNOLOGISCHE FORSCHUNG MBH. DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                                Fraser CM,
Timmis KN,
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FT misc_feature complement (3574937144) FT /*tag= am /note= "AT2" FT misc_feature complement (3714538296) FT /*tag= an /note= "KS2" FT misc_feature complement (3837138581) FT misc_feature complement (3867739307) FT misc_feature complement (3867739307) FT misc_feature complement (3867739307) FT misc_feature complement (3967739307) FT misc_feature complement (3967739307)	FT misc_feature (7005= "DH1"  FT misc_feature (7005= "DH1"  FT misc_feature (70001-0001)  FT Mote= "Red Gomain"  FT Mote= "Red Gomain"  FT Mote= "Red Gomain"  FT Mote= "Red Gome"   FT Mote= "Red Gome"   FT Mote= "Red Gome"	misc_feature 56019  *tag= nisc_feature 57710  misc_feature 57710  misc_feature 57710  *tag= nisc_feature 57990  *tag= nisc_feature 59244  misc_feature 59344  /*tag= nisc_feature 60399  /*tag= //*tag= //*tag
	complement (1782019053) /*tag= s /*tag= s /*tag= t /*tag= t /*tag= t /*tag= t /*tag= t /*tag= u /*tag= v /*ta	/*tag= ad //*tag= ad /note="ACP3" /*tag= ae /note="KR3" /*tag= af /note="DH3 (inactive)" /*tag= ag /note="AT3" /*tag= ag /note="AT3" /*tag= ah /note="KS3" /*tag= ah /note="KS3" /*tag= ai /note="KS3" /*tag= ai /note="KR2" /*tag= ai /note="KR2" /*tag= ai /note="KR2" /*tag= ai /note="KR2" /*tag= ai /note="KR2" /*tag= ai /note="KR2" /*tag= ai /*tag= ai
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FT /product- "Protein of ORF 7" complement (1275110829)	CDS	FT /*tag= i FT /product= "Protein of ORF 9" FT CDS complement (15203.13614)	CDS	CDS	f ORF	CDS (58266530) (*tag= 0 /radiate	CDS	CDS	CDS	CDS COMPleme	/*tag= /product CDS compleme	/*tag= u //tag= u //tag= complement (7542474213)	/*tag= v /*tag= v /product= "Protein of ORF 75535.76464 /*tag= w /	CDS	CDS Complement (7986478107)	cDS	CDS COMPLEME	CDS	<del>7</del> , w	/product= "Protein of ORF 29" CDS 84481.18548 /*tad= ad	£ 0 5
Db 48334 GCCGCCCTGCCGAACTGCCGCTTGCCGGTGCAGTACGCCGACTTCGCCGCCTGGGAG 48393  Qy 123 AAGGACCAATTCATAGAGCAGGAGAAGCAACTCAACT	CGCGCCCGGACTGGACAGCGCTACTGCCGACCAACTC 48453	Qy 177AAAGACTCTTCCCCAGCAAGATCCCGACCGACTTTGCCCGCCC	293	294 TTCTGCAACGAACAACAACGACCTCTTTCGTCGTTCTTCTAGCTGCGGTCCTCACG 485/3  48574 CTCGCACCAACAACAACAACAAAAAAAAAAAAAAAAAAA	354 CATTATCGTCTCACAGCTGTTCATGACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	473	533		•	781 standard; DNA; 88421 BP.	AAL40781; 03-OCT-2002 (first entry)	88421nt genomic DNA of ramoplanin producing Actinoplanes sp.	KW Ramoplanin; ramoplanin biosynthetic pathway polypeptide; antibiotic; FT FT KW biosynthesis gene cluster; bioengineering; peptide synthetase module; FT FT RW adenylation domain; hydroxyphenylglycine; HPG; antibiotic precursor; FT FT Chlorinate; lipdepsipeptide; gene; ds.	Actinoplanes sp.	FH Key Location/Qualifiers FT FT CDS 2077.3078 FT	/*tag= a //*tag= a //*tag= CDS	/*tag= b /product= "Protein of ORF 2" 40385048	CDS	/*tag= d /product= "Protein of ORF 4" CDS complement (77036693)	CDS	FT //rag= 1 FT //rag= 1 FT //rag= 9611.10761 FT //tag= 9 FT //tag=

59487 GGGTGCCGGCCGAGGTGCACCTGGCCGAGCTGGCCCGGTCCGAGGGGCGTGACCG 59546

59547 TGTTCATGGTGCTGCAGGCCGCCTTCGGCACGCTGCTGTCCCGCCTCGGCGCCCCGGCGCGCG 59606

CTTTCGTCGTTCTTCTAGCTGCGTTCCGTGCCGCTCATTATCGTCTCACACAGCTGTTGAAG

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GCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATCATCACGATACCTTTGGGA 498

59607 ACATCCCGATCGCCACGGCGGTCGCCGGCCGCACCACCAGGCCCTCGACGAGCTCGTCG 59666

ACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGGACCTGAACTGGAGGATATCATCG

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499 CTTTGATCAACCAAGTCAAGGCTACGACGACAGCAGCATTCGAGAACGAGGATATTCCGT

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bloomgineering of antibloids structures. An isolated polypeptide or its encoding nucleic acid sequence is useful for generating derivatives of ramoplanin, for improving production or for producing variants of other antibiotics of the peptide class. The isolated polypeptides are useful for synthesis of ramoplanin in vivo or in vitro, as an adenylation domain in conjunction with other peptide synthetase modules and allowing the incorporation of Thr into a peptide antibiotic precursor, for modifying fatty acid structure and/or enhancing fatty acid incorporation into the peptide antibiotic structure, for production of an hydroxyphenylglycine (HPG)-containing peptide antibiotic, for enhancing secretion of ramoplanin or its variants and derivatives, for enhancing uptake of precursors for ramoplanin blosynthesis, for enhancing production of ramoplanin products or its variants or derivatives, to chlorinate HPG of a peptide antibiotic precursor, and for designing specific nucleotide probase and primers for identifying and isolating putative lipdepsipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide selected from a polypeptide of open reading frames (ORF)
1-32. The isolated polypeptides are useful for chemically modifying a
blological molecule that is a substrate for a polypeptide encoded by
ramoplanin blosynthesis gene cluster, by contacting the blological
molecule with the isolated polypeptide, where the polypeptide chemically
modifies the blological molecule. The method comprises contacting the
blological molecule with at least two different polypeptides encoded by
amoplanin ORFs 1-31. The polypeptides are useful for directing the
blosynthesis of the antibiotic ramoplanin in microorganisms. An isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO22152, AAO22153, AAO22154, AAO22155, AAO22156, AAO22157, AAO22159, AAO22159, AAO22161, AAO22161, AAO22161, AAO22161, AAO22161, AAO22161, AAO22161, AAO22161, AAO22171, AAO22171, AAO22173, AAO22173, AAO22171, AAO22172, AAO22173, AAO22173, AAO22173, AAO22173, AAO22173, AAO22173, AAO22173, AAO22178, AAO22177, AAO22178, AAO22177, AAO22178, AAO22177, AAO22178, AAO22178, AAO22177, AAO22178, AAO221778, AAO22178, AAO22188, AAO28188, AAO28188, AAO28188, AAO28188, AAO28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ECOP-) ECOPIA BIOSCIENCES INC.
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24-JUL-2001; 2001US-0910813.
87372..86803
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   CDS
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Bacillus subtilis; Iturin A; cation channel; ds.

Bacillus subtilis

JP2001231561-A.

28-AUG-2001.

Bacillus subtilis Iturin A.

15-JAN-2002 (first entry)

AAI66165;

18-FEB-2000; 2000JP-0040825 18-FEB-2000; 2000JP-0040825

AAI66165 standard; DNA; 41599 BP.

RESULT 14 AAI66165

59787 TCGAGCGGCTCGT 59799

TTGAGCGCGTTGT 571

559

A gene encoding Iturin A for the production of large amounts of Iturin

WPI; 2001-642167/74

(MASA/) MASADA M.

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TCCCGACCGACTTTGCCCGCCCTGCACTTCTGTCTGGAGACGCCAGGTTGCGTACATGTTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a gene encoding Iturin A encoding a protein having an activity of promoting the transfer of a cation to the exterior of the cell through the cation channel of the cell and a promoter for transferring the cation to the exterior of the cell containing Iturin A as the active component. The gene can be used for the preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 41599;
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Pred. No. 4.5e-09;
0; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 4-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as the active component. The Iturin A in a large quantity.
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Matches 180; Conservative
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Length 88421; Indels

Score 65.8; DB 24; Pred. No. 2.1e-09; 0; Mismatches 192;

6.6%;

Local Similarity 48.5 es 181; Conservative

Best Loca Matches

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Query Match

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                                                   13307 CCTTACAGCCGGATGTCATCCGTTCCAGACTTGGCGCCAAAAGGCGGAAACGACTC 13366
                                                                                                                           13367 TCTATACAGTGCTGCTGCCCCTATAATGTGCTTCATAATATAATATACGGGACAAGAG 13426
                                                                                                                                                                                        13547 ATTATCTGGAAGAAGTAAAGCGGCAGACGCTTGACGCTTTCGAAAACCAAGACTATCCAT 13606
             CCATCGACGCGAGCTCTACCAGTCCCTTCGAGCCTTCTGCAACGAACACAACACGACCT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a fragment of the cyclosporin synthetase gene from T. geodes. This fragment was isolated using primers derived from the Tolypocladium niveum (formerly known as T. inflatum GAMS) cyclosporin synthetase gene, corresponding to bases 35073-35092 and 37848-37829. The T. niveum gene encodes an enzyme which catalyses the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37848-37829. The T. niveum gene encodes an enzyme which catalyses the peptide biosynthesis of cyclosporins and structurally related molecules. The T. niveum sequence may be used for the production of cyclosporin by transforming a vector containing the gene sequence in
                                                                                      319 CTTTCGTCGTTCTTGTAGCTGCGTTCCGTGCCGCTCATTATCGTCTCACAGCTGTTGAAG
                                                                                                                                                                 379 ACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGACCTGAACTGGAGGATATCATCG
                                                                                                                                                                                                                                          GCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATCATCACGATACCTTTGGGA
                                                                                                                                                                                                                                                                                                                  CTTTGATCAACCAAGTCAAGGCTACGACGACAGCAGCATTTCGAGAACGAGGATATTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum;
T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated DNA sequence - which codes for enzyme having cyclosporin synthetase like activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T. geodes Cyclosporin synthetase gene fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANO ) SANDOZ LTD.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
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93CH-0001310.
93CH-0001375.
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                                                                                                                                                                                                                                                                                                                                                                                             TTGAGCGCGTTGT 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Folypocladium geodes
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29-APR-1993;
04-MAY-1993;
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to a recombinant host. This allows effective production of antibiotic cyclosporin or its derivatives.
                                                                                                                                                                              387 ATTGGTACACCAATTGCGAATCGCAACCGACCTGAACTGGAGGATATCATCGCTGCTTT
                                                                                                                           Gaps
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                                                                                      Length 178;
                                                                                    Score 62.8; DB 15; Length
Pred. No. 5.5e-10;
0; Mismatches 62; Indels
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                                                 Sequence 178 BP; 49 A; 39 C; 43 G; 47 T; 0 other;
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illarity 61.7%;
Conservative
                                                                                                   Similarity
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Job time: 290.5 secs
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Matches 100;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435 ATTONNEY AGENT INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERNCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFRAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS: US-08-254-021-97
US-08-618-446-97
US-08-618-446-97
US-09-585-798-97
US-09-585-719-3
US-08-1719-1
TITLE OF INVENTION: Cyclosporin Synthetase NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: US-08-340-011-3 US-08-901-710-3 5: No. 5827706artis Corporation 59 Route 10 ALIGNMENTS Sequence 1, Application US/08471119A
Patent No. 5827706
GENERAL INFORMATION:
APPLICANT: Leitner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Syn COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO LENGTH: 46899 base pairs 807 807 807 1395 3601 3601 4405 44195 4416 4416 4416 single STREET: 59 Route 10 CITY: East Hanover STATE: New Jersey COUNTRY: USA nucleic acid unknown STRANDEDNESS: ANTI-SENSE: NO ORIGINAL SOURCE 07936 ADDRESSEE: TOPOLOGY: US-08-471-119A-1 0 0 0 0 0 0 0 0 0 0 0 0 0 Sequence 1, Appli Sequence 3, Appli Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 3, Appli Sequence 24, Appl (without alignments) 5385.674 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence 17, 1 Sequence 2, 1 Sequence 1, 1 US-09-482-788-1\_COPY\_4000\_5000 1001 1 caattgatgtcttgcgacgc........cccaagtctctgcttacccc 1001 Sequence 2, Sequence 1, Description Sequence Sequence Sequence Sequence 3 Sequence Sequence Sequence Sequence Sequence June 4, 2003, 19:04:47; Search time 57 Seconds Issued\_Patents\_NA:\*

'cgn2\_c/ptodata/1/ina/5A\_COMB.seq:\*
'cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
'cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
'cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
'cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
'cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
'cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\* GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. US-09-103-840A-2 US-09-103-840A-1 US-08-510-646B-17 US-09-103-840A-2 US-09-103-840A-2 US-08-222-617A-24 US-08-743-200-5 US-08-452-655B-1 US-08-450-582-1 US-07-741-940-1 US-08-289-548A-1 US-08-403-852D-14 US-08-510-646B-14 US-09-231-818-14 Total number of hits satisfying chosen parameters: US-08-222-617A-3 441362 seqs, 153338381 residues SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 seq length: 0 seq length: 200000000 Query Match Length DB Scoring table: Title: Perfect score:

Length 46899;

Score 339.4; DB 1; Pred. No. 2.2e-101;

33.9%; 60.1%;

Query Match Best Local Similarity

US-08-471-119A-1

Sequence

Sequence Sequence Sequence

Sequence

US-08-961-527-3 US-08-961-527-77 US-07-706-691G-97

PCT-US95-04228-17

US-08-446-648-17

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ORGANISM: Tolypocladium niveum STRAIN: ATCC 34921

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387 ATTGGTACACCAATTGCGAATCGCAACCGACCTGAACTGGAGGATATCATCGGCTGCTTT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 GTCAATACGCAGTGTATGCGAATCAACATAGATCATCACGATACCTTTGGGACTTTGATC 506
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Pred. No. 3.5e-11;
0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFAX: 201 503 8807
                                                                  APPLICANT: Schneider, Elisabeth
APPLICANT: Schoergendorfer, Kurt
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827706artis Corporation STREET: 59 Route 10
                                                                                                                                                                                                                                                                                                                                                                  US/08/471,119A
                                                                                                                                                                                                                                                                                                                  SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08403852D Patent No. 5891695
   Sequence 3, Application US/08471119A
Patent No. 5827706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tolypocladium geodes
                                                                                                                                                                                                                                                                                     Eloppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blanche, Francis
Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.3%;
Best Local Similarity 61.7%;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995
                                                      Leitner, Ernst
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: .178 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                    East Hanover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                      Patent No. 5827706
GENERAL INFORMATION:
APPLICANT: Leitne
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APPLICANT: Blanc,
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06
CLASSIFICATION:
                                                                                                                                                                                                                                     USA
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                                                 30283 ATCCGTTATCTCAGGTCAAGCCCCTCCCAATACAATATCGTGACTTTGCGGCTTGGCAGA 30342
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                                                                                               64 ACCCGCTGTCAGCACTCCTCTACCTATCCAGTACAGCGACTTTGCAAAATGGCAGA
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 Mismatches
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 Conservative
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Gaps

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Indels

RESULT 2 US-08-471-119A-3

Jacques, Nathalie Lacroix, Patricia Thibaut, Denis

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TITLE OF INVENTION: Polypeptides Involved In The TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                                                                   335 AACTCGTCGCACGCGTGCGCCACTTCGACCTCGCCGCCTACACACCACCAGGACATGCCGT 394
499 CTTTGATCAACCAAGTCAAGGCTACGACACGACAGCATTCGAGAACGAGGATATTCCGT
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1300 I Street, N.W., Suite 700
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE PAPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
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                                                                                                                                               559 TTGAGCGCGTTGTATCAGCACTACAGCCTG 588
                                                                                                                                                                                         395 TCGAAAAGCTCGTCGAAGAGGTCAACCCCG 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08510646B Patent No. 6077699
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Debussche, Laurent
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REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Patricia
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                                                                                                                                                                                                                                                                                                                                                               Blanc, Veronique
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denis
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CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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STATE: D.C
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APPLICANT:
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             Debussche, Laurent
De Crecy-Lagard, Valerie
VENTION: Polypeptides Involved In The
VENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
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1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/403,852D FILING DATE: 10-MAY-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/FR 93/00923 FILING DATE: 25-SEP-1993 PRIOR APPLICATION DATA: RPLICATION NUMBER: FR 92/11441 FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                2: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14:
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  Zagorec, Monique
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LENGTH: 474 base pairs
                                                       TITLE OF INVENTION: POTENTIALE OF INVENTION: BLOSTITLE OF INVENTION: COAL NUMBER OF SEQUENCE: 43 CORRESPONDENCE ADDRESS:
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Matches 184; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                       USA
                                                                                                                                                                   ADDRESSEE:
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US/08/403,852

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10-MAY-1995
APPLICATION NUMBER:
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APPLICANT:
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TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                            199 TCCCGACCGACTTTGCCCGCCCTGCACTTCTGTCTGGAGACGCAGGTTGCGTACATGTTA 258
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1300 I Street, N.W., Suite 700
                                                                                             Length 474;
                                            /product= "Partie du gene SnbD'
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                                                                                           .4; DB 3;
4e-10;
                                                                                                                             206;
                                                                                                                             0; Mismatches
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                                                                                             6.0%; Score 60.4; 47.2%; Pred. No. 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09231818 Patent No. 6171846
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Zagorec, Monique
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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FILING DATE:
PRIOR APPLICATION DATA:
                           LOCATION: 1..474 OTHER INFORMATION:
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APPLICANT: Blanc,
                                                                                             Query Match
Best Local Similarity
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APPLICANT:
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Pred. No. 4e-10;
0; Mismatches 206;
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                                                         MBER: PCT/FR 93/00923
25-SEP-1993
                                                                                                                                                                                        FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 47.2%;
Matches 184; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
FILING DATE: 10-MAY-19
APPLICATION NUMBER: PC
FILING DATE: 25-SEP-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR
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OTHER INFORMATION:
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GENERAL INFORMATION:
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ADDRESSEE:
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US-08-510-646B-17
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APPLICANT:
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNMARE: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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Pred. No. 1e-07;
0; Mismatches 201;
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; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis FEATURE:
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Patent No. 629423
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                              CTHER INFORMATION: CDC 1551
CTHER INFORMATION: "n" bases at
CHER INFORMATION: represent a,
US-09-103-9408-2
                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%;
Best Local Similarity 47.4%;
Matches 181; Conservative
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                   LENGTH: 4403765
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SOFTWARE:
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2663182 TCATCAACATCGTGGTGTTGCGCAACGACCTGCGCGGGAACCCCACGCTGCGCGAGGTGC 2663123
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                                                                                                                                                                                                   TCGTTCTTCTAGCTGCGTTCCGTGCCGCTCATTATCGTCTCACAGCTGTTGAAGACGCTG
                                                                                   205 CCGACTTTGCCCGCCCTGCACTTCTGTCTGGAGACGCAGGTTGCGTACATGTTACCATCG
                                                                                                                                                                                                                                                                                                                                                 385 TCATTGGTACACCAATTGCGAATCGCAACCGACCTGAACTGGAGGATATCATCGGCTGCT
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                                               Gaps
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  Length 4411529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garrett & Dunner
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Score 60.4; DB 4;
Pred. No. 1e-07;
0; Mismatches 201;
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                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0,
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Thibaut, Denis
Zagorec, Monique
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6.08;
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                                          181; Conservative
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COMPUTER READABLE FORM:
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APPLICANT: Blanc,
                      Best Local Similarity
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Sequence 1, Application US/09103840A Patent No. 6294328
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: FLEISCHMAN, Robert D.
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Best Local Similarity 47.3%;
Matches 142; Conservative
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                    Similarity
                                                           SEQ_ID NO 2
LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       817 ACCTGGAGCCCGAGCTGCACGAGCGGCTCAGCGCCTGGCCAGGTCCTGCGAGCCCAGCC 876
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APPLICANT: FRASER, Claire M.
APPLICANT: VERSER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product = "virginiamycin s synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2219;
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Pred. No. 1.8e-07;
0; Mismatches 209;
                                                                          NAME: Meyers, Kenneth J.
REGIGSTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.48;
                                    FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: s. virginiae
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Best Local Similarity 46.1
Matches 179; Conservative
                                                                                                                                                                                                                                                          nucleic acid
EDNESS: double
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; OTHER INFORMATION:
US-08-510-646B-17
                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                            TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
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HYPOTHETICAL: 1
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                                                                                                      OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 GCTCTACCAGTCCCTTCGAGCCTTCTGCAACGAACACAACACACGACCTCTTTCGTCGTTCT
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VERWER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 CURRENT FILING DATE: 1998-06-24 COPPURABLE CONTINUED OF SEQ ID NOS: 2
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Pred. No. 0.0025;
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Pred. No. 0.0024;
0; Mismatches 158; Indels
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TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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387 ATTGGTACACCAATTGCGAATCGCAACCGACCTGAACTGGAGGATATCATCGGCTGCTTT
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TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 ATTGGTACACCAATTGCGAATCGCAACCGACCTGAACTGGAGGATATCATCGGCTGCTTT
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43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURREMY APPLICATION DATA:
APPLICATION WABER: US/08/222,617A
FILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 8050 .8052
COTHER INFORMATION:
COTHER INFORMATION: /note= "NNN=AGU, AGC, UCU,
NOTE: 1780-222-617A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

4.1%; Score 41.2; DB 2;
Best Local Similarity 60.9%; Pred. No. 0.0064;
Matches 67; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 388..11526
OTHER INFORMATION: /function= "Enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
FEATURE:
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                          Sequence 24, Application US/08222617A Patent No. 5882879
                                                                                                                                                                                                                                                                                                                       Veenstra, Annemarie E.
Martin, Juan F.
Garcia, Bruno D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van Liempt, Henk
Montenegro, Eduardo P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                Gutierrez, Santiago
Barredo, Jose L.
Von Doehren, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 11601 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Palissa, Harriet
67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90909
                                                                                                                                                                                                                      RESULT 12
US-08-222-617A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
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  Matches
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                                                                                                     512 AGTCAAGGCTACGACGACGAGCATTCGAGAACGAGGATATTCCGTTTGAGCGCGTTGT 571
                                                                             452 TACGCAGTGTATGCGAATCAACATAGATCATCACGATACCTTTGGACTTTGATCAACCA 511
392 TACACCAATTGCGAATCGCAACCGACCTGAACTGGAGGATATCATCGGCTGCTTTGTCAA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "NNN=GCC, AGU, AGC, UCU, UCC, UCA, or UCG;
Xaa=Ala or Ser "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Liempt, Henk
Montenegro, Eduardo P.
Wontenegro, A Method for Influencing Beta-Lactam
VENTION: A Method for Influencing Acta Isolation of Large
VENTION: Quantities of ACV Synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 11601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: U4-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41.2; DB 2;
Pred. No. 0.0064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /function= "Enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97,157
                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08222617A Patent No. 5882879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Veenstra, Annemarie
APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutierrez, Santiago
                                                                                                                                                                                                                                                                                                                                                                                                                                       Barredo, Jose L.
Von Doehren, Hans
Palissa, Harriet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
REFERENCE/CDCKET NUMBER:
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 11601 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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388..11526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
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STREET: 300
TTWY: Chicago
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                                                                                                                                                                                                                                                                               US-08-222-617A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8052 GTCAATCACCGGGGGGGTTTACCTGTGGGAGATCTTCCAGATCTAGGATTGT 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  940 TCGACTATCCCCGAGAATCGAGCTTGGCTGATGTCTTCCAGACCCAAGTCTCT 992
                                                                                 APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKANDRA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 8532;
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
FILING DATE: 25-M31-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%; Score 33; 55.8%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                        ADDRESSEE: Banner & Witcoff, Ltd. STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08450582
Patent No. 6114124
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                           CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8532 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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            ANAND, RAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMMEDIATE SOURCE:
CLONE: DP2.5(APC)
                                                                                                                                                                                                                                                                                                                Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-450-582-1/c
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                                                                                                                                                                                                                                                                                                                CITY: STATE:
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7189 GTCAACTTGCTCCCTCTGCGGGTCAACGTGTTCAGGTCGGACATTCATGG 7238
                                                          447 GTCAATACGCAGTGTATGCGAATCAACATAAGATCATCACGATACCTTTGG 496
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                                                                                                                                                                                                                                                             APPLICANT: DOXSEY, Stephen J.
TITLE OF INVENTION: DIAGNOSTIC METHODS FOR SCREENING
TITLE OF INVENTION: PATIENTS FOR SCLERODERMA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFFLANCE
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32.983
REFERENCE/DOCKET NUMBER: 07917/025001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.3%; Score 33; DB
ilarity 69.2%; Pred. No. 0.38
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: CASTEM: DOS
SUFTWARE: FRASES VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,200
PRIOM APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY
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Sequence 1, Application US/08452655B
Patent No. 278366
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
                                                                                                                                                                                                       Sequence 5, Application US/08743200 Patent No. 5861260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coding Sequence 3...329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02110-2804
                                                                                                                                                                                                                                               GENERAL INFORMATION:
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US-08-743-200-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                  US-08-743-200-5
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STATE:
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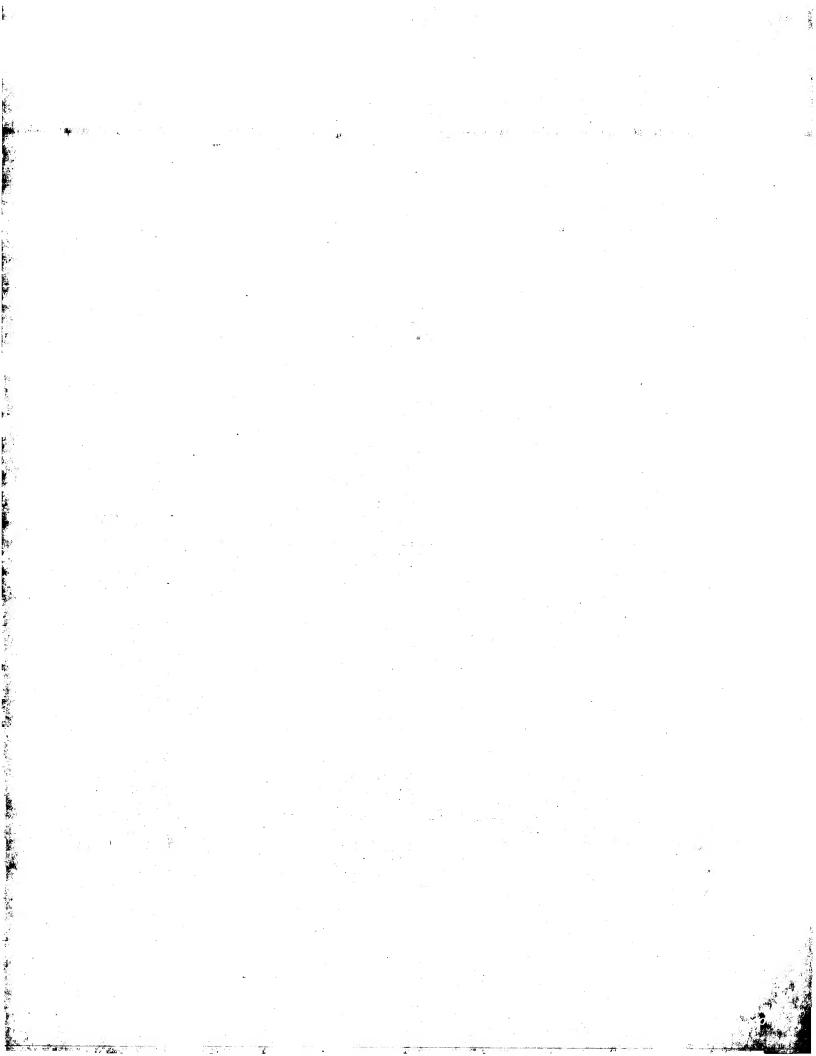
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ANAND, RAKESH

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880 TTCCTTTGACTGATGGCATTGTGACTCTTGAAAAATTGGATGTTCTCAACGTCAAACATG 939
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                                           APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
ITILE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
ITILE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.3%; Score 33; DB 3; Length 8532; Best Local Similarity 55.8%; Pred. No. 2.8; Matches 63; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY,AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ. 100
TELEFAR. 202-508-9299
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                         ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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MOLECULE TYPE: c
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: USA
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Search completed: June 4, 2003, 21:50:58 Job time: 93 secs



Thu Jun

Published\_Applications\_NA:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		•				
Result		Query				
No.	Score	Match	Match Length DB	BB :	ID	Description
Н	75.6	7.6	13029	10	US-09-815-242-4052	Sequence 4052, Ap
	71.8	7.2	3471	10	US-09-974-300-2167	Sequence 2167, Ap
e	65.8	9.9	88421	σ	US-09-976-059-1	Sequence 1, Appli
4	60.4	0.9	7347	10	US-09-815-242-7773	Sequence 7773, Ap
2	56	5.6	7158	10	US-09-974-300-2171	Sequence 2171, Ap
9	47.2	4.7	6465	10	US-09-974-300-2166	Sequence 2166, Ap
7	47.2	4.7	8268	10	US-09-974-300-2169	Sequence 2169, Ap
8	41.6	4.2	693	6	US-10-123-155-406	Sequence 406, App
σ	34.8	3.5	473	6	US-09-918-995-31196	Sequence 31196, A
10	34.8	3.5	558	6	US-09-918-995-28625	Sequence 28625, A
11	34.2	3.4	269	10	US-09-923-876-5113	Sequence 5113, Ap
12	33.8	3.4	175561	σ	US-10-017-721-3	Sequence 3, Appli
c 13	33	3.3	10383	10	US-09-960-253-181	Sequence 181, App
14	32.8	3.3	6827	10	US-09-982-610-17	Sequence 17, Appl
c 15	32.6	3.3	1290	10	US-09-815-242-7834	Sequence 7834, Ap
c 16	32.2	3.2	2277	6	US-10-189-971-21	Sequence 21, Appl
c 17	32.2	3.2	3173	6	US-10-189-971-5	Sequence 5, Appli
c 18	32.2	3.2	3753	σ	US-10-189-971-15	Sequence 15, Appl
c 19	32.2	3.2	4026	σ	US-10-189-971-23	Sequence 23, Appl

	Sequence 1682, Ap Sequence 1379, Ap Sequence 1, Appli
9 US-10-189-971-9 9 US-10-189-971-11 9 US-10-189-971-11 9 US-10-189-971-12 10 US-09-913-876-5115 10 US-09-915-876-5115 10 US-09-1564-2158 10 US-09-298-764-869-2158 10 US-09-298-5084-1027 10 US-09-908-500A-1 10 US-09-908-500A-1 10 US-09-908-501A-1 10 US-09-912-610-31 10 US-09-912-610-31 10 US-09-912-610-45 10 US-09-912-610-45	10 US-09-974-300-1682 10 US-09-867-550-1379 10 US-09-824-567-1
4536 4710 4710 266 285 913 913 1160 1159 470 471 4711 4415 49744 49744 49744	1314 1711 1799
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3322.2 3222.2 32	30.4 30.4 30.4
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## ALIGNMENTS

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APPLICANT: HASELDECK, KODETL
APPLICANT: Chisen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: DEPORTYOUS
FILE REPRENCE: ELTERA.011A
CURRENT APPLICATION NUMBER: G0/191, 078
PRIOR APPLICATION NUMBER: G0/205, 848
PRIOR PLICATION NUMBER: G0/206, 848
PRIOR APPLICATION NUMBER: G0/206, 848
PRIOR PLICATION NUMBER: G0/205, 848
PRIOR APPLICATION NUMBER: G0/205, 848
PRIOR PLICATION NUMBER: G0/205, 878
PRIOR FILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: G0/253, 625
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: G0/253, 838
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-26
PRIOR PLILING DATE: 2000-11-27
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SOFTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 4052
LENGTH: 13029
                                   Sequence 4052, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-4052
                                                                                                                        GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
US-09-815-242-4052
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Score 75.6; DB 10; Length 13029; Pred. No. 4.5e-14;

7.6%;

Query Match Best Local Similarity

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1462 AAAACGGCGGCGACATTGTACATGGTCATGCTGTCTGCGTACAACATGCTTCTTGCAAAGT 1521
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OTHER INFORMATION: ORF 10; negative strandedness
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OTHER INFORMATION: ORF 4; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (9464)..(8130)
OTHER INFORMATION: ORF 6; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (9691)..(10761)
OTHER INFORMATION: ORF 7; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (13617)..(12802)
OTHER INFORMATION: ORF 9; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     positive strandedness
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                                                                                                                                                                                                                                                                                            544 ACGAGGATATTCCGTTTGAGCGCGTTG 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Actinoplanes sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (4038)..(5048)
OTHER INFORMATION: ORF 3;
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LOCATION: (7703)..(6693)
OTHER INFORMATION: ORF 5;
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OTHER INFORMATION: ORF 1;
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OTHER INFORMATION: ORF 2;
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OTHER INFORMATION: ORF 3;
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LOCATION: (4038)..(5048
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LOCATION: (13617)..(128
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LOCATION: (6665)..(581
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LOCATION: (12751)..(10
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US-09-976-059-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5966 GCTACAGCGGCCAGCAGGACCTGCGTATCGGCGCGCGGCGGTGGCGAACCGCATCCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 AACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATC
                                                                                                                       AAGACCCGCTGTCAGCACTCCTCTCTACCTATCCAGTACAGCGACTTTGCAAAATGGC
                                                                                                                                                              5666 AATCGCCGCTGGAGCCGTTGCCGGTCCAGTACCTGGACTACAGCGTGTGGCAGCGCGAGT
                                                                                                                                                                                                        241 CAGGTTGCGTACATGTTACCATCGACGCGAGCTCTACCAGTCCCTTCGAGCCTTCTGCA
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                                        1 CAATTGATGTCTTGCGACGCGATCTCAATCAGCTCTACTCAGCTGCGCTCAAGGACTCAA
    Gaps
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Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT FILING DATE: 2001-10-05
PRIOR PLICATION NUMBER: 09/680,598
PRIOR PLICATION NUMBER: 09/680,596
PRIOR PLICATION NUMBER: 09/680,596
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILOR DATE: 2000-10-06
PRIOR PLILOR DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
  Mismatches 319; Indels
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0; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4:0
SEQ ID NO 2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2167
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54.38;
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267;
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Best Local
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1582 TGGAAGGAATCATCGCCATGTTTGTCAATACGCTGGCGATCCGTTCAAAAGTGGACCCGG 1641
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                                                                                                                             TGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATCATC 483
                                                                                                                                                                                                                                                             484 ACGATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACAGCAGTTCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1. Application US/09976059
Patent No. US20020164747A1
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Sazopoulos, Emmanuel
APPLICANT: Sazopoulos, Emmanuel
APPLICANT: Gardfa, Alfredo
TITLE OF INVENTION Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
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LOCATION: (15591)..(15863)
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1534 TGCCGTACGATTITCCGCGGCCTTCAAAACGCAGCTTTGAAGGCGACCGTGTCGTCTTTG 1593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1654 TTTATATATGTTCCTGTTGGCCGCGTTTAATATTTTGCTGTCCAAGTATGCGTCTCAGGAAG 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1834 AATTTTTGCAGGAAGTCAAAGAGACAAGTCTTCAGGGCTTTGCCAAGCAGGACTATCCGC 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCTTTGTCAATACGCAGTGTATGCGAATCAACATAGATCATCACGATACCTTTGGGA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 TCCCGACCGACTTTGCCCGCCCTGCACTTCTGTCTGGAGACGCAGGTTGCGTACATGTTA
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                                                                                Indels
                                                                                                                                                                                                                                     GENERAL IN-CORNATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
AITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 0201-10-05
PRIOR APPLICATION NUMBER: 0201-10-05
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2169, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Mady M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
                                                           543 AACGAGGATATTCCGTTTGAGCGCGTTGTATCAGCACTACAGCC
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Pred. No. 0.00013;
0; Mismatches 198;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2166
                                                                                                                                                                                                   Sequence 2166, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus licheniformis. US-09-974-300-2166
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Best Local Similarity 45.6%;
Matches 166; Conservative
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                                                                                  871 TTGCTGGCTTCGTTCCAGCGCTGCTGTATCGTACTCGTGTC
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                                                         270 GAGCICTACCAGICCCITCGAGCCITCIGCAACGAACACACACACGACCICITICGICGIT
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Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: BERKA, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
ed. No. 4.6e-09;
Mismatches 166;
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1.4e-07;
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CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
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SEQ ID NO 2171
LENGTH: 7158
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Pred. No.
Pred. No.
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US-09-974-300-2171
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49.18;
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Best Local Similarity 47.7%
Matches 164; Conservative
                   Conservative
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Best Local Similarity
Matches 160; Conserv
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US-09-974-300-2171
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Pred. No. 0.00016;
0; Mismatches 198;
            FILE REFERENCE: 10085.500.US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PELING DATE: 2000-10-06
PRIOR PELING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: RESUSED for Windows Version 4.0
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US-09-974-300-2169
  Expression
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sal Similarity 45.6%;
166; Conservative
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Goddard, Audrey
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Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
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Gurney, Austin L.
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Filvaroff, Ellen
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Best Local Similarity
Matches 166; Conserv
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TTGA 1598
TITLE OF INVENTION:
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US-10-123-155-406
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LENGTH: 8268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 GEAEKRLLLVDFSSQALFQDKNSSQVLGEKVLGIVVQNTKVANLTEPVVLTFQHQLQPKN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630 TTTGCAGTGCACTCACAGAAGGACCTTGGAAGATTCAAGTTCCAGGGTCTCGAGTCCGTA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::::::| | | ::::::| | | 462 YESLLSYVGCVVSALACLVTIAAYLCSRVPLPCRRKPRDYTIKVHMNLLLAVFLLDISFL 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750 GACAGCCTTAAAGGTAGCGTCAACTTTGCCGATGAGCTGTTCAAAATGGAGACTGTTGAA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     810 AATGTCGTCAGAGTATTCTTTGAGATTCTGAGAAACGGGCTTCAAAGTTCGCGGACACCA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 VTLQCVFWVEDPTLSSPGHWSSAGCETVRRETQTSCFCNHLTYFAVLMVSSVEVDAVHKH 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 LSEPVALIGSEAGCRASAIFLHFSLLTCLSWMGLEGYNLYRLVVEVFGTYVPGYLLKLSA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522 MGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDSLVSYITNLGLFSLV 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLFNMAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLGLPWALIFFSFASGTFQLVVLY 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               690 CCTGTGCCTAGCAAAGCGTACACTCGATTTGACATGGAGTTCCAFCTGTTTCAAGAAACC
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                                                                                                                                                                                                                                                                                                                                      Length 693;
                                                                                                                                                                                                                                                                                                                                   Query Match 4.2%; Score 41.6; DB 9; Length 6 Best Local Similarity 10.1%; Pred. No. 0.0025; Matches 40; Conservative 119; Mismatches 238; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hyeary, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR PILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930 GTCAAACATGTCGACTATCCCCGAGAATCGAGCTTGG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 LFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDS 678
                                                                                             See Palm or File Wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
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58.8%; Pred. No. 0.41;
tive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
                                     US/10/123,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31196, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31196
                                                                 2002-04-15
FILE REFERENCE: P3330R1C30
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2002-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5
Best Local Similarity 58.8
Matches 60; Conservative
                                                                                             Prior Application removed NUMBER OF SEQ ID NOS: 550
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo Sapien
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162 ACTICCGCCAAAGCCTICGICCAAGCIGNCCGACAIGGAGAICGAIGAAIGCCGAGGGGC 221
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                                                                                                                                                                                            629 TITIGCAGTGCACTCACAGAAGGACCTTGGAAGATTCAAGTTCCAGGGTCTCGAGTCCGT
                                                                                                                                                                                                                                        102 TITCACGGTGGAGTICCCCGACTCGCTGGCACCAGAGCAGTGCAAGGNICTCGAGTCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Daley, George
APPLICANT: Daley, George
APPLICANT: Bolk, Stacey
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MAIL-003
CURRENT APPLICATION NUMBER: US/10/017,721
CURRENT APPLICATION NUMBER: US 60/317,033
PRIOR APPLICATION NUMBER: US 60/310,248
PRIOR FILING DATE: 2001-09-04
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTERO for Windows Version 4.0
                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.556
CURRENT APPLICATION NUMBER: US/09/960,253
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Indels
                                                                                                 Score 34.2; DB 10;
Pred. No. 0.45;
0; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33.8; D
Pred. No. 41;
0; Mismatches
                               g, or other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10017721
Publication No. US20030096248A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.4%;
                                                                                                 Query Match 3.4%;
Best Local Similarity 54.5%;
Matches 66; Conservative
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                               t,
c,
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nes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-017-721-3
    ) LOCATION: 149, 190
) OTHER INFORMATION: a,
US-09-923-876-5113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: McCarthy,
                                                                                                                                                                                                                                                                                                                                                                                 749 C 749
                                                                                                                                                                                                                                                                                                                                                                                                                               C 222
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LENGTH: 175561
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Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalgudi, Radhunath V.

APPLICANT: Lalgudi, Radhunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT APPLICATION NUMBER: 09/298,329

PRIOR PAPLICATION NUMBER: 09/298,329

PRIOR PILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL Program
140 GCAGGAGAAGCAACTCAACTACTGGAAGAAGCAACTCAAAGACTCTTCCCCAGCAAAGAT 199
                                              287 GCAGAAAAAACCAAAAAACTACAAAACAAAAGCAGCCCTCTGCCTCCTCCCCCAGGGAAGAC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 GCAGGAGAAGCAACTCAACTACTGGAAGAAGCAACTCAAAGACTCTTCCCCCAGCAAAGAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GCAGAAAAAAAAAAAAACTACAAAAAAGCAGCCCTCTGCCTCCCCCCAGGGAAGAC 220
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OTHER INFORMATION: Incyte ID No. US20020013958A1 700456379H1
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PAPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTESQ FOR WINDOWS Version 3.0
                                                                                                                       200 CCCGACCGACTTTGCCCGCCCTGCACTTCTGTCTGGAGACGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 CCCGACCGACTTTGCCCGCCCTGCACTTCTGTCTGGAGACGC 241
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58.8%; Pred. No. 0.45;
Live 0; Mismatches 42;
                                                                                                                                                                                                                                                         Sequence 28625, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-28625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
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US-09-923-876-5113
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LENGTH: 269
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2486 GTCACTCTGCGTGGTGTACACCTTGTCGAAGATGCTTTCAGGGGCCATCCACTTCAGGGG 2545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 GCCGCTCATTATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAAT 407
                                                                                                                                                                                                           408 CGCAACCGACCTGAACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTGTATGCGA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 TCCCGACCGACTTTGCCCGCCCTGCACTTCTGTGTGGAGACGCAGGTTGCGTACATGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       782 TCCAGGTCGTACTTGCCGTCCTTGAAGAACTCGCTGGAGGCGCCAGGTCCAGGGCCAGGGTC
                                     Length 6827;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                67;
                                         DB 10;
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Pred. No. 4.4;
0; Mismatches
                                       Score 32.8; DI
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/227
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7834
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7834, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                      2606 AAAGTCACAGATCTTCACCA 2625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                              468 ATCAACATAGATCATCACGA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamancto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%;
                                         3.3%;
52.1%;
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APPLICANT: Haselbeck, Robert
                                                                                   Conservative
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US-09-815-242-7834
                                         Query Match
Best Local Similarity
Matches 73; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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JS-09-815-242-7834/c
US-09-982-610-17
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Best Local S
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                                                                                                                                                                                                                                                      Gaps
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                           Score 33; DB 10;
Pred. No. 12;
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                                                                                                                                                                                                                                                    0; Mismatches
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APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

PREJICATION NUMBER: 08/46,648
FILING DATE: 1996-WAY-23
APPLICATION NUMBER: 08/22616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                        9519, 10205
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                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 9089, 9347, 9453, 9519,
OTHER INFORMATION: n = A,T,C or G
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Matthews, William
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Bennett, Brian D.
Goeddel, David
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Wood, William I
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Best Local Similarity 55.8%;
Matches 63; Conservative
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                                                        ORGANISM: Homo sapiens
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SEQ ID NO 181
                                       TYPE: DNA
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3.7 492 12 BF653686 3.7 493 12 BF653730 3.7 280 12 BF665366 3.7 586 12 BF646516 3.7 662 12 BF644804 3.7 662 12 BF644804 3.7 663 10 AW689667 3.7 591 9 AIT37351 3.6 338 10 AW656085 3.6 816 10 BE64080 3.6 816 10 BE64080 3.6 816 10 BE64080 3.6 816 10 BE64080 3.6 736 17 CNSO7LBT 3.6 736 17 CNSO7LBT 3.6 736 14 BH75905 3.6 736 14 BH55436 3.5 208 14 BH751536	3.5 1000 14 3.5 720 1101 117 3.5 748 117 3.5 938 140 13 3.5 1031 111 3.5 1031 111 3.5 248 12 3.5 248 12 3.5 340 9 3.5 648 10 3.5 648 10 3.5 648 10 3.5 648 10 3.5 648 10 3.5 648 10 3.5 648 10	ALIGNMENTS  AQ989462  Rfc00006 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG00006, DNA sequence. AQ989462. GSS. Photorhabdus luminescens. Photorhabdus luminescens. Photorhabdus luminescens. Photorhabdus. 1 (Abses 1 to 438) Ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000) Contact: ffrench-Constant RH Department of Biology and Biochemistry Contact: ffrench-Constant RH Department of Biology and Biochemistry South Building, Bath Fel: (44) 1225 826521 Fmail: bssrfc6bath.ac.uk This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
	225 226 227 228 239 239 231 239 239 239 239 239 239 239 239 239 239	1 FION TION OS WISM NISM NISM NISM NISM IN
	000 0 0 00 00	RESULT AQ9894 LOCUS LOCUS DEFINI ACCESS VERSION KEYWORI SOURCE ORGAL AUTH TITL JOUR MEDL COMMEN
on 5.1.6 3 Compugen Ltd. 1.1 Search time 1708.5 Seconds (without alignments) 9488.839 Million cell updates/sec. 5000cccaagtctctgcttacccc 1001	hits satisfying chosen parameters: 32308132 hits satisfying chosen parameters: 32308132 ength: 0 ength: 0 ength: 0 ength: 0 ength: 0 ength: 45 summaries  EST:* 1: em_estba:* 2: em_estbu:* 3: em_estbu:* 4: em_estpu:* 5: em_estpu:* 6: em_estp:* 7: em_estp:* 8: em_estp:* 9: gb_est:*	results predicted by chance to have a to the score of the result being printed, of the total score distribution.  SUMMARIES  SUMMARIES  A0989462 A0980256 A0990256 A0990256 A0991640 BF036321 BE130762 BM012777 BM012777 BM012777 BM012777 BM012777 BM012777 BM012777

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/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00996"
                                                                      library"
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Photorhabdus.
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Best Local S.
Matches 112
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                                                                                                                                                                                                                                                                                                                                                    351 GCTCATTATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCCAATTGCGAATCGC 410
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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
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/note="Genomic DNA from strain W14 was size selected
kb) and then cloned into M13 Janus."
93 c 149 g 104 t
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                                                                                                 /strain="W14"
/db_xref="taxon:29488"
/db_xref="taxon:29488"
/clone="PLG00006"
/clone_lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                                                                                                                                                  Length 438;
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    .438
/organism="Photorhabdus luminescens"

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Pred. No. 6.8e-09;
0; Mismatches 106;
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Acids Res.
Seq primer: M13 Forward
Class: shotgun.
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Best Local Similarity 55.1%;
Matches 130; Conservative (
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/organism="Photorhabdus luminescens"

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AQ991640 1inear GSS 14-AUG-2000 RfC01385F Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01385F, DNA sequence.
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(figurent-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                   selected (1-2
                                                                                                                                                                                                                                                                                                                                                                                                     358 ATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACCAATTGCGAATCGCAACCGAC 417
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Photorhabdus luminescens .
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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/clone_lib="Photorhabdus luminescens strain W14
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                                                                                                                                                                                                                                                                         Length 637;
                                                              /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size
kb) and then cloned from strain W14 was size
124 c 134 g 211 t 2 others
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Pred. No. 0.26;
0; Mismatches 117; Indels
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Contact: ffrench-Constant RH
Department of Bailogy and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 846621
Feax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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                                                                                                                                                                                                                                                                  tch 4.2%; al Similarity 48.9%; 112; Conservative
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100 ACAGCGACTTTGCAAAATGGCAGAAGGACCAATTCATAGAGCAGGAGAAGCAACTCAACT
                                                                                                                       160 ACTGGAAGAAGCAACTCAAAGACTCTTCCCCAGCAAAGATCCCGA 204
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92; Conserva
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/ Organism="Homo sapiens"
/ Adb.xref="taxon:9606"
/ Clone="taxon:9606"
/ Clone=1ib="NIH_MGC_66"
/ Lissue_type="adenocarcinoma"
/ Lab_host="UH10B (phage-resistant)"
/ note="Organ: overy; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life
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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus." 173 c 210 g 187 t 45 others
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                                                                                                                                                                                                                                                           89 ATTGCGTATGGATTTATCGGGTGAACTGACCGTGACCGAGTTGCTGGCGCGAGCCCGGCA 148
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                                                                                                                                                       401 TGCGAATCGCAACCGACCTGAACTGGAGGATATCATCGGCTGCTTTGTCAATACGCAGTG 460
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NIH-WGC http://mgc.nci.nih,gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601459544F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863075 5',
                                                                                                                                                                          29 TGCAGGCCGTAATCGTCAGGAAGTAGATGGTTGATTGGTCTTTGTCAATACGTTGGC
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                                                                                                                                                                                                                                                                                                                 149 AATCGCATTGACGCGCAGGAGCATCAGACTTACGATTGAACAGGTGGTGGAAATCGT
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Pred. No. 0.82;
0; Mismatches 91;
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Plate: LLAM9602 row: g column: 12
High quality sequence stop: 397.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Best Local Similarity 51.1%;
Matches 95; Conservative
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Best Local Similarity 52.19
Matches 86; Conservative
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XR expression library
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L48-973T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-973 5',
                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae, Caryophyllidae; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 786)
Cushman, J.C.
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/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone="L48-973"
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Pred. No.
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University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 350
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Unpublished (1997)
Contact: Cushman JC
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High quality se
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ilarity 51.9%;
Conservative
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                                                                                                                                                                                                                                                     BM012777 791 bp mRNA linear EST 30-OCT-2001 603637492F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5459759 5',
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  714 GGTCTTTAATGAAACTGATTAAAATGAAGGAAGCTATAGCCAAATGGGAGAAATTTTCGA 773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (20 791)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs.remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1963 row: g column: 24
High quality sequence stop: 285.
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                                                                                                                                                                                                                                                                                                                                                                     BM012777.1 GI:16527131
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                                                                                                                                                                                                                                                                                                                mRNA sequence.
BM012777
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Best Local Similarity
Matches 69; Conserv
                                                       AA 795
                                                                                                               AA 775
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LOCUS
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AUTHORS
TITLE
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KEYWORDS
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RESULT 7 BF653686/c

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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Gasas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Keele, J. W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: NotI: Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 CTGGTCATAGAAAACACCCTTTTCCAACACAAGAGACAACTCTACACATGGACATCACA 306
                                                                                                                                                                    Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     674 GGGTCTCGAGTCCGTACCTGTGCCTAGCAAAGCGTACACTCGATTTGACATGGAGTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         734 TCTGTTTCAAGAAACCGACAGCCTTAAAGGTAGCGTCAACTTTGCCGATGAGCTGTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 492;
DF003086 492 bp mRNA linear 277599 MARC 3BOV Bos taurus cDNA 5', mRNA sequence. BF653686
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277659 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF653730
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.2; DE
Pred. No. 5.6;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 66 row: F column: 24
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus'
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 9
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VERSION
KEYWORDS
SOURCE
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USA

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Anotes Weetor: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Torres-Jerez, I. Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
                   Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 bp mRNA linear EST 20-DEC-2 NF076F01EC1F1013 Elicited cell culture Medicago truncatula cDNA BF646516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Cell cultures derived from root tissues" /dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 CCCTTCGAGCCTTCTGCAACGAACACAACACGACCTCTTTCGTCGTTCTTCTAGCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 TCCGTGCCGCTCATTATCGTCTCACAGCTGTTGAAGACGCTGTCATTGGTACACTTG
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                                                                                                                                                                                 The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, Tel: 580 221 7302 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Elicited cell culture"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF010A02EC"
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Unpublished (2000)
                                                                                        Center for Medicago Genomics Research
                                                                                                                                                                                                                                                                        Email: radixon@oble.org
Insert Length: 280 Std Error: 0.00
Plate: 010 row: A column: 02
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
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Pred. No. 5.1;
0; Mismatches
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                                                                                                                                      Contact: Dixon RA
Plant Biology Division
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55.5%;
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(bases 1 to 280)
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                                                                                                              Unpublished (2000)
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Best Local S
Matches 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                 1 (bases 1 to 493)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
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Medicago truncatula
Medicago truncatula
Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 CTGGTCATAGAAAACACCCTTTTCCAACACAAGAGACAACTCTACACATGGACATCACA 307
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            734 TCTGTTTCAAGAAACCGACAGCCTTAAAGGTAGCGTCAACTTTGCCGATGAGCTGTTCAA
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                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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51.9%; Pred. No. 5.6;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: P column: 24
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
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                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
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                                                                                                              AUTHORS
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LOCUS
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Indels 0; Gaps

57;

Length 280;

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EST 20-DEC-2000

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/organism="Medicago truncatula"
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1. .483

/organism="Medicago truncatula"
/db_xref="taxon.3880"
/clone="ntroof for the call culture"
/clone="ntroof for the call cultures derived from root tissues"
/clone="lib="Blicited cell cultures derived from root tissues"
/fissue_type="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taxen at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from time point were pooled and used for mRNA isolation."

111 c 105 g 134 t 2 others
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7331
Fax: 580 221 7331
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 586 Std Error: 0.00
Plate: 095 row: E column: 06
Seq primer: TCACAGGARACAGCTATGAC.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586 bp mRNA linear EST 16-MAR-2
NF095E06LF1F1040 Developing leaf Medicago truncatula cDNA clone
NF095E06LF 5', mRNA sequence.
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2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Flisert Length: 483 Std Error: 0.00
Plate: 076 row: F column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
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Pred. No. 7.3;
0; Mismatches
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Best Local Similarity 55.5%;
Matches 71; Conservative
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source

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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores-Jeres, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research Unpublished (2000)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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//clone_lib="Elicited cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 an
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
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NF022H10EC1F1091 Elicited cell culture Medicago truncatula cDNA
Clone NF022H10EC 5', mRNA sequence.
                                                                                                                                                       very
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                      /tissue_type="leaf"
//dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
young, developing, mature and senescing leaves."
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0
                                                                                                                                                                                                                                                                                                      Length 586;
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7380
                                                                                                                                                                                                                                                                                                   Score 36.8; DB 12;
Pred. No. 8.3;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Medicago truncatula"
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/db_xref="taxon:3880"
/clone="NF095E06LF"
/clone_lib="Developing leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: radixon@oble.org
Insert Length: 662 Std Error: 0.00
Plate: 022 row: H column: 10
Seq primer: TCACACAGGAAACAGTATGAC.
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Best Local Similarity 55.5%;
Matches 71; Conservative 0
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AI737351 591 bp. mRNA linear EST 02-FEB-2000 606039D04.x1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.

AI737351. GI:5058875
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1; Poales; Poaceae; PACC
 155 TCGCTTCCGGTTACATCCTCACCGCTACTGGTCCTCAAGCTCTCTGATACCGCTCTTT 214
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/clone_l1b="606 - Ear tissue cDNA library from Schmidt
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/lab_host="XLOLR (Stratagene)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbottestanford.edu
Plate: 606039 row: D column: 04.
Location/Qualifiers
ce 1.591
/organism="Zea mays"
/organism="Zea mays"
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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Walbot, V.
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Matches 90; Conservative
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                                        403 CGAATCGC 410
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                               283 CCCTTCGAGCCTTCTGCAACGAACACACACGACCTCTTTCGTCGTTCTTCTAGCTGCGT 342
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
.C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000) Contact: Dixon RA
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/db_xref="taxon:3880"
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/clone=lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="weetor: Lambda Zap; Contains a mixture of internodal stem segments"
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7380
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ilarity 55.5%; Pred. No. 9.1;
Conservative 0; Mismatches 57;
                                                                     57;
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Insert Length: 668 Std Error: 0.00
Plate: 025 row: c column: 03
Seg primer: TCACACGGAAACAGCTATGAC.
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Pred: No. 9;
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Malbot,V. Malbot,V. Malbot,V. Malbot,V. Maize ESTs from various cDNA libraries sequenced at Stanford University
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Directionally sequenced with 5' end at the EcoRI site.
Created by Amle Franklin."
138 c 180 g 159 t 1 others
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/cultivar="0hio43"
/cultivar="0hio43"
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/dev_stage="premieotic anthers to pollen shed"
/lab_host="xLour"
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                                                                                                                                                                                                                         Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 821
Email: walbot@stanford.edu
Plate: 660004 row: A column: 04.
Location/Qualifiers
ce 1. 639
                         Zea mays.
Zea mays
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Search completed: June 4, 2003, 21:48:21 Job time: 1717.5 secs

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4, 2003, 17:30:47; Search time 2758 Seconds (without alignments) 10562.693 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES æ

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ALIGNMENTS

RESULT 1

PLN 11-SEP-2001

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Fusarium scirpi esynl gene for enniatin sythetase. 218755. 3 GI:15591913 enniatin sythetase; esynl gene. Fusarium equiseti. Fusarium equiseti. Eukarvium equiseti. FSESYN1A LOCUS DEFINITION ACCESSION VERSION VERSION SOURCE ORGANISM REFERENCE

AUTHORS TITLE

Hapocreales, mitosporic Hypocreales; Fusarium.

(bases 1 to 10934)

Haeses, A., Schubert, M., Herrmann, M. and Zocher, R.

Molecular characterization of the enniatin synthetase gene encoding a multifunctional enzyme catalysing N-methyldepsipeptide formation

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Submitted (11-SEP-2001) Zocher R., Technische Universtaet Berlin,
Mar- Volmmer- Institut fuer Biophysikalische Chemie und Blochemie,
Abteilung Biochemie und Molekulare Biologie Sek. OE2, Franklinstr.
29, D-10587 Berlin, GERMANY
On Sep 12, 2001 this sequence version replaced gi:7327885.
                                                                                                                                                                                                                                                                                                                                                   Zocher, R. Direct Submission Direct Submission Direct Submission Submitted (22-MAR-2000) Zocher R., Technische Universtaet Berlin, Max Volmer - Institut fuer Biophysikalische Chemie und Biochemie, Abteilung Biochemie und Molekulare Biologie Sek. OE2, Franklinstr. 29, D-10587 Berlin, GERMANY Revised by [5]
                                                                                                                                                                      Direct Submission
Submitted (24-NOV-1992) Haese A., Technische Universtaet Berlin,
Institut fuer Biochemie u. Mol. Biologie, Franklinstr.29, W-1000
Berlin 10, F.R.G
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GACCCCTTCAGCGACTGCAAAACCGTCGTATCGCCATCGAAGTCCGCGAGAGGTTCGGT
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Nonribosomal Biosynthesis of N-methylated peptides in fungi
Unpublished
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Submitted (17-WAR-1995) Burmester J., Universitaet Zuerich,
Biochemisches Institut, Winterthurer Str. 190, Zuerich,
Switzerland, CH - 8057
On Oct 25, 2001 this sequence version replaced gi:732698.
Location/Qualifiers
1. 2949
/organism="Gibberella pulicaris"
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Highly conserved N-methyltransferases as
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/db_xref="taxon:5128"
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             624
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Mido.N., Okakura.K., Miyamoto,K., Watanabe,M., Yanai,K.,
Mido.N., Okakura.K., Miyamoto,K., Watanabe,M., Yanai,K.,
Wasutake,T., Aihara,S., Futamura,T., Kleinkauf,H. and Murakami,T.
Cyclic depsipeptide synthetase and its gene and mass production
system of cyclic depsipeptide
Batcht: Wo 0118179-A 1 15-MAR-2001;
MEIJI SEIRA KAISHA LTD. NAOKI MIDO, KAORU OKAKURA, KOICHI MIYAMOTO,
MANABU WATANABE, KOJI YANAI, TETSUYA YASUTAKE, SATO AIHARA, AKAFUMI
FUTAMURA, HORST KLEINRAUF, TAKESHI MURAKAMI
OS Mycella sterilia
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                                      GCCCTCTTCAGAAGCTGCAGCGCCGTCGTGCCGCTTTGCAAGTCCGCGAAAGTCTCCAGT
                                                                                                                                                                                                                                                                                             CCTTACTTCCATCGTACATGATCCCATCGAACATCGTTGTTCTGGACAAGATGCCTCTCA
                                                                                                                         ACGCCAATGGTAAAGTTGACCGGAAGGAACTCTCTCGCAGGGCAAAGGTTGTACCGAAGC
                                                                                                                                                                              745 AGCAGACAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTCATTCTTTGCG
                                                                                                                                                                                                                                      805 AAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACTTCTTCAATCTCG
                                                                                                                                                                                                                                                       GTATCACTGTCAAGGATGTCTTTGACCATCCTGTATTTGCGGATCTAGCATCTGTCATCC
           GACCCCTTCAGCGACTGCAAAACCGTCGTATCGCCATCGAAGTCCGCGAGAGGTTCGGT
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07-SEP-1999 JP 99P 253040,06-APR-2000 JP 00P 104291
I MIDO,KAORU OKAKURA,KOICHI MIYAMOTO,MANABU WATANABE, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETSUYA YASUTAKE, SATO AIHARA, TAKAFUMI FUTAMURA, HORST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Location/Qualifiers
1. .9633
/organism="unidentified"
/db_xref="taxon:32644"
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KLEINKAUF,
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qq	7860 TCGTGTCTGTGAGGGATGTTCGACCAGCCTGTGATTTCCGACCTCGCAGTCACCCT 7919	qa	7020 GGAACAGTCGCGGCCCGTGTATCCGATCCAAGTGAACGACTGGATCGACTTTCAGGCCTC 7079
δ	CCGTCAAGGGCTGGGTTTG		TCAATTGAACCAGAAGTCACTGGGGGGCCTTCTCAAGTCTTCAGATGCTGCTATCAT
Dp.	7920 CCGCCAGGGACTGACCTTG 7938	QQ	7080 ACGCATTGACCGCCGCGCCCTTCTCCGACTCCTACAGCGCTCGGCAGACGCCGGGGCGGT 7139
RES BD0		Qy	254 GGCAGTCAGCAAAATTCCTTTCGAAATCACGGCCTTTGAAAGACAGGTCGTCGCTTCCCT 313 
3 X X I	BD010086; Scandard; DNA; 9033 BF.		CAATAGCAACATCGATGAGTGGCAGCTATCAAC
SV	BD010088.1		TGACAATAACAACAGGAGAATACGCATAGAGCACCAGACGGCGCGCGC
X L L S	08-FEB-2002 (Rel. 70, Created) 08-FEB-2002 (Rel. 70, Last updated, Version 1)	Qy Db	347 CATICGETCCAGCCCAGGGCGACTCATCACTATCCGTTCCCGACATCTTTCGCATTGC 406 1
YE DE Y	Cyclic depsipeptide synthetase and its gene and mass production system of cyclic depsipeptide.		TGGGGAAGCCGGGTTCCGTGTCGAGTTCTGCACACACAGTGGTCTCAGAATGGTGC
X X X	JP 03075848-T/1.	oy Oy	467 ATTGGACGCTGTTTTCCATCATGTTGCTCCCAAGGCGTACTTCTGGT 514
88\$	unluchtlied unclassified.	qq	7380 GCTCGATGCCGTCTTTCACCGCTATAATTTGCCCACTCAAAGCAATAGTCGCGTTCTGAT 7439
RN RA	[1] 1-9633 Mido N., Okakura K., Miyamoto K., Watanabe M., Yanai K., Yasutake T.,	Qy	515 CAACTTTCCTACGGACCATCACCTTCGAGGTCTGATCTCCTCACCAATCGACCCCT 571
RRRE	Athara 5., Futamura T., Kleinkaui H., Murakami T.; "Cyclic depsipeptide synthetase and its gene and mass production system of cyclic depsipeptide"; Patent number JP03075848-T/1, 06-MAR-2001.	Qy Dp	572 TCAGGGACTGCAAAACCGTCGTATCGCCATCGAAGTCCGGGAGAGGCTTCGGTCCTTACT 631
3888		Qy Db	632 TCCATCGTACATGATCCCATCGAACATGTTCTGGACAAGATGCCTCTCAACGCCAA 691 
8888	PD 06-MAR-2001 PP 07-SEP-2000 JP 2000006103 PR 07-SEP-1999 JP 99P 253040,06-APR-2000 JP 00P 104291 PI NAOKI MIDO,KAORU OKAKURA,KOICHI MIYAMOTO,MANABU WATANABE,	Oy Db	692 TGGTAAAGTTGACCGGAAGGAACTCTCGCAGGGCAAAGGTTGTACCGAAGCAGAC 751 
8888	H	۷۶ و	752 AGCAGCGCCGTTACCGACATTCCCATCAGTGAGGTCGAAGTCATTCTTG 802 7680 GCF   1   1   1   1   1   1   1   1   1
888	PC C12N9/00,C12N15/52,C12N1/15,C12P21/04	3 6	CGAAGAAGCCATGAGGTTTTGGCATGAAGGTTGACATTACGGATCACTTCAATCT
8888	FH Key Location/Qualifiers FT CDS (1). (9633) FT mat_peptide (13). (9630)	q <sub>Q</sub>	TGAGGAGTTCGCGGAGGTCGCATGGCGCGCGCGCGCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCAACTTCCACTTCACTT
XX FH FH	Locat	Qy Db	863 CGGTGGACACTCTCTTGGCCACGAAGCTCATTCTCGTATCGACCAACGACTCAAGGT 922 
FT	source 19633 /db_xref="taxon:32644" /organism="unidentified"	Oy	
os S	Sequence 9633 BP; 2318 A; 2834 C; 2462 G; 2019 T; 0 other;	<u>a</u> .	ICGIGICIGIGAGGGGAIGIGITCGACCAGCCIGIGAITICCGACCICGCAGCCIC
OME	Query Match 28.2%; Score 282.6; DB 23; Length 9633; Best Local Similarity 59.5%; Pred. No. 6.6e-75; Matches 618; Conservative 0; Mismatches 364; Indels 57; Gaps 6;	, da	983 CCGCCAGGGGTTTG 1001 - 1
Oy Db	20 GTTGAAAGACAGGTTTCCAGGTCTGGAACATGTTGAGATCCTGCCAAAGAACATGGA 79	RESULT 5 A36768 LOCUS	A36768 46899 bp
oy d	80 AGCTGTGAATGAGCTCAGTGCGTATGGATATGCCGCTGTTGTGCACGTTCGGGGTTCACT 139	DEFINITIO ACCESSION VERSION KEVWODDS	Sequence 1 Irom Patent A36768 A36768.1 GI:2294035
QY		SOURCE	Tolypocladium inflatum. M Tolypocladium inflatum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

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PAT 29-SEP-1999
                                                                AGCAGCAGCAGCACCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTCATTCTTT
                                                                                                             GCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACTTCTTCAATC
                                                                                                                                                                         862 TCGGTGGACACTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTCAAGG
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Leitur. E., Schneider.E., Schoergendorfer,K. and Weber,G.
Cyclosporin synthetase
Patent: US 5827706-A 1 27-OCT-1998;
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Pred. No. 7.5e-62;
0; Mismatches 418;
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10651 a 13511 c 12510 g 10227
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1 from patent US 5827706. AR050554 GI:5973279
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Best Local Similarity 55.0%;
Matches 563; Conservative 0
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22093 TCC 22095
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Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
                                              Weber, G
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                         l (bases 1 to 46899)
Leitner,E., Schneider,E., Schoergendorfer,K. and Cylosporin Synthetase
Patent: Ep 0578616-A 1 12-JAN-1994;
SANDOZ LTD (CH)
Other publication JP 6225773 940816
Other publication AT 43793 940515
Other publication AT 398578 941227
Other publication AT 398434 941227
Location/Qualifiers
                                                                                                                                                                                                               /organism-"Tolypocladium inflatum"
/Astrain-"ATCC 34921"
/Ab_xref-"taxon:29910"
13511 c 12510 g 10227 t
                                                                                                                                                                                                                                                                                                          Score 240.2; DB 6;
Pred. No. 7.5e-62;
0; Mismatches 418;
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RRRLQMLLPSYMMPARIVVLDHLPLNPNGKVDRKALGQSAKTVQKSKLVSQRVAPRNE
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SAALRGQDPLSRLEPLPIQYRDFAVWQKQDSQQKAAHQRQLEYWTKQLADSTPAELLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSTGKPKGVMIEHRGVLRLVKQTNILSSLPPAQTFRMAHMSNLAFDASIWEVFTALLN
GGSLVCIDRFTILDAQALEALFLREHINIALFPPALLKQCLTDAAATIKSLDLLYVGG
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LLVDPAFFTSLKESLSEEIEHVEIILPKNMKVNNELSSYRYGAVLHIRNHNQNQSRSIH
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YMIPARIVVLQNMPLNTSGKVDRKELTLRAKVTAARTPSSELVAPRDSIEAIICKEFK
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EHRGIVRLTKQTNITSKLPESFHMAHISNLAFDASVWEVFTTLLNGGTLVCIDYFTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDSRSLDIIQQELGELYTAASQGKSISACPLGPIPIQYRDLTTWQNQDEQVAEQERQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELERMGLLHMVKTDYPRNMSVVDVFQQQVRLSAEATAVIDSSSRMSYAELDQRSDQV
AAWLRQRQLPAETFVAVLAPRSCEAVIALFGILKAGHAYLPLDVNVPAARLRAILAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGEKLVLLGAGEPSPEGQSPEVSIVRIADATSPAGHASLRDGKSKPTAGSLAYVIFTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLERGLRIVDASSRDLAQLLAEEQTMKFDLESEPAWRVALLKVAEDHHILSIVVHHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFEQVVSSLMPSSSRDASRNPLVQLMFALHGQQDLFKIQLEGTEEEVIPTEEVTRFD.
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                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="mgaig@dmaydrlanpsrassissnrysepvegsfaggrlwf
QLKLGASWDITPPAAIRLRGHLDIDALNAASRALTQRHETLRTTFKEQDGVGVQVVH
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                                                                                                                                                                                                                                                                                                        /product="cyclosporine synthetase"
/protein_id="CAA82227.1"
/db_xref="G1:440169"
                                                      organism="Tolypocladium inflatum"
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:Q09164"
                                                                                                                                                                                                                                                                                    /evidence=experimental
                                                                                                          /db_xref="taxon:29910"
  Jocation/Qualifiers
                                                                                /strain="ATCC3492
                                                                                                                                                                                                                                                       'codon_start=1
                                                                                                                           /gene="simA"
885. ArT
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/gene="simA"
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Submitted (29-NOV-1993) Weber G., Biochemie Ges. m.b.H., Molekulare
Genetik 2, Kufstein-Schaftenau, Austria, A-6330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISACYS 46899 bp DNA linear PLN 06-DEC-1994 inveum (ATCC34921) simA gene for cyclosporine synthetase.
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                                                                                                                                                                                                                          --CGTACTCTGGTCAACTTTCCTACGGACCATCACCTTCGAGGGTCTGATCTCCTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGACCCCTTCAGCGACTGCAAAACCGTCGTATCGCCATCGAAGTCCGCGAGAGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21676 ACCGTCCCCTGAACAGCATTCAAAGCCGCCGTCTTGGGACGCAGATCCGCGAGAAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGTTGTTCTGGACAAGATGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAACGCCAATGGTAAAGTTGACCGGAAGGAACTCTCTCGCAGGGCAAAGGTTGTACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 742 AGCAGCAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTCATTCTTT
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                                                                                                                                                                                             GGTCTCAGAATGGTGCATTGGACGCTGTTTTCCATCATTGTTGCTCCCAAGGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide synthetase; synA gene.
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Hypocreales; Clavicipitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyclosporine synthetase;
Tolypocladium inflatum.
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NIPYSKTVVERHIVRSLDQEDANAPEESMDGSDWISAVRTRAQCCHTLSASDLFDIAE
DAGFRVEVSARARQHSQHGALDAVFHHKFATEDESNLJKFFPTHQGRFKSLTNQPLL
PAGSRRAELLIREGLQTLLPPYMIPSQITLIDRWPLNANGKVDRRELARRAKITOKSK
PVEDIVPPRNSVEATVCKGFTDVLGVEVGITDNFFNLGGHSLMATKLAARLGRQLNTR
TSRRDVFDOEVVADLAAVIQNRSAPHEBIRARAKTGPVFDVLDKFNLGGHSLMATKLARFDGLNYGAT
WYLMPLGIRLHGSLRYDALAAVIASALSALSQRHPELRATTGPFEDGUVGAT
TDLSTQPRDAXLAAVLKHEQTTLFDLATEPGWRVALIRLGEEEHILSIVMHHISDGWS DHQGRPEEALTNHPLHRAQSRRVERQIRERLQTLLPAYMIPAQIMVLDKLPLNANGKV DRKQLTQRAQTVPKAKQVSAPVAPRTEIERVLCQEFSDVLGVDIGIMENFFDLGGGHSL MATKLAARISRRLETHVSVKEIFDHPRVCDLVLIVQQGSAPHDPIVSTKYTGPVPQSF FQEILRRGLNGPDVPISTLPLQDGIVDLQRQGLLDVQKTEYPRDSSVVDVFHEQVSIN PDSIALIHGSEKLSYAQLDRESDRVARWLRHRSFSSDTLIAVLAPRSCETIIAFLGIL KANLAYLPLDVKAPAARIDAIVSSLPGNKLILLGANVTPPKLQEAAIDFVPIRDTFTT QGLTSDMAVINSVAQYFPTPEYLAETIKSLVQVPGMKRIYLGDMRSWAWNRDFAARA AYSLADNASKDRVRQKMMELEEKEEELLVDPAFFTALASQLQDRIQHVEILPKRWKAT NELSSYRYAAVLHISDEPLPIYKIDPEAWINFEGSRLTREALAQVLKENENAESVAIS TATSAFANQDVPFESIVSSLLPGSRDASRNPLVQVILAVHSQODLGKLTLEGLRDEAV DSAISTRFDVEFHLFEHADRLSGSVLYAKELFKLRTIESVVSVFLETLRRALDQPLTP LAVLPLTDGVGEIASKGLLDVPRTDYPRDANIVEVFQQHVRATPDAIAVKDATSILTY AQLDQOSDRLAIWLSRRHMMPETLVGVLAPRSCETI IÄMFGIMKANLAYLPLDINSPA ARERSILSAVOGNKLVLLGSGVTAPBOSDRPVEVASVGIQELLAGYGLDERFOSA TSLAAVUIFTSGSTGRFKGVAVENTRAREN SNVI SKLPQGARVAHLANIABDASIM EĻATTLLNGATLVCLDYHTVLDCRTLKEVFERESITVVTLMPALLKQCVAEIPETLAH RSLLDSQPPGHVLEVGTGTGMVLFNLGREGGLQSYVGLEPSPSATAFVNKAAKSFPGL EDRIRVEVGTATDIDRLGDDLHAGLVVVNSVAQYFPSQDYLAQLVRDLFKVPGVERIF FGDMRSHAINRDFLVARAVHALGDKATKAEIQREVVRMEESEDELLVDPAFFTSLTTQ VENIKHVEILPKRMRATNELSSYRYAAVLHVNDLAKPAHKVSPGAWVDFAATKMDRDA LIRLLRGTKISDHIAIANIPNSKTIVERTICESVYDLGGDAKDSNDRVSWLSAARSNA VKVASLSAIDLVDIAQEAGFRVEISCARQWSQNGALDAVFHHLGPSPQSSHVLIDFLT AQGRLWFLDQLNFGATWYLMPLAVRLRGAMNVHALTAAALLALERRHELLRTTFYBONG VGMQKVNPVVTETLRIIDLSNGDGDYLPTLKKBQTAPFHLETEPGWRVALLRLGPGDY ILSVVMHHIISDGWSVDVLFQELGQFYSTAVKGHDPLSQTTPLPIHYRDFALWQKKPT VHRVTSFVVLLAALRAAHYRLTGSEDATIGTP IANRNRPELEQIIGFFVNTQCIRITV NEDETFESLVQQVRSTATAAFAHQDVPFEKIVSTLLPGSRDASRNPLVQLMFAVHSQK NLGELKLENAHSEVVPTEITTRFDLEFHLFQQDDKLEGSILYSTDLFEAVSVQSLLSV LTDGTLQDGPTIERPSAQSLAYAMFTSGSTGRPKGVMVQHRNIVRLVKNSNVVAKQPA AARIAHISNLAFDASSWEIYAPLLNGGAIVCADYFTTIDPQALQETFQEHEIRGAMLP PSLLKQCLVQAPDMISRLDILFAAGDRFSSVDALQAQRLVGSGVFNAYGPTENTILST IYNVAENDSFVNGVPIGSAVSNSGAYIMDKNQQLVPAGVMGELVVTGDGLARGYMDPK QAFLNDGFVEDVAIVIRTPENQEPEMVAFVTAKGDNSAREEEATTQIEGWEAHFEGGA YANIEEIESEALGYDFMGWTSMYDGTEIDKDEMREWLNDTMRSLLDGKPAGRVLEVGT VEVLFDEMHRFYSSALRQQDPMEQILPLPIQYRDFAAWOKTEEQVAEHORQLDYWTEH LADSTPAELLTDLPRPSILSGRANELPLTIEGRLHDKLRAFCRVHQATPFVILLAALR AAHYRLTGAEDATLGTPIANRNRPELENMIGFFVNTQCMRIAIEENDNFESLYRRVRS DFMGWTSMYDGSEIDKTDMHEWLNDTMRMILDAREPGHVLEIGTGTGMOWFNLAKCPG LQGYVGFEPSKSAAQFVNDAAQSFPALKDGRSIVHVGTATDINKAGPIQPRLVVINSV AQYFPTPEYLFRVVEALVQIPSVERIVFGDMRTNAINRDFVASRALHTLGEKANKRLV VRGSREQSTIHQVSPNAWIDFAADGLDRQTLINLLKEHKDAGTVAIGNIPYSKTIVER FVNKSLSEDDMEEGQNSLDGSAWVAAVRMAAQSCPSLDAMDVKEIAQEAGYQVEVSWA REKLOTLLPPYMIPSRIMVLDQMPVNNNGKIDRKELVRRAIVAPKPRSAATRVAPRNE IEAILRDEFEDVLGTEVSVLDNFFDLGGHSLMATKLAARVSRRLDAHISIKDVFDOPV LEVLRREQTVPFDLSSEPGWRVCLVKTGEEDHVLSIVMHHIIYDGWSVDILRGELGQF YSAALRGQDPLLHANPLPIQYRDFAAWQREAKQVEEHQRQLGYWSKQLVDSTPAELLT FHLVPGDQKLTGSVLYSSDLFEQGTIQNFVDIFQECLRSVLDQPLTPISVLPFSNAIS NLESLDLLEMPTSDYPRDRTVVDLFREQAAICPDSIAVKDSSSQLTYAQLDEQSDRVA QESEHERQLQYWVEQLVDSAPAELLTDLPRPSILSGQAGEMSVTIEGALYKNLEEFCR LDADRFIQLTVNGSEQVRAYRTGDRVRYRPKDFQIEFFGRMDQQIKIRGHRIEPAEVE **GTGMIMFNLGRSQGLERY IGLEPAPSAAEFVNNAAKSFPGLAGRAEVHVGTAADVGTL** LÖLLYTGGDRVGGHDAMRARSLVKIGMFSGYGPTENTVISTIYEVDÄDEMFVNGVPIG KTVSNSGAYVMDRNQQLVPSGVVGELVVTGDGLARGYTDPSLNKNRFIYITVNGESIR AYRTGDRVRYRPHDLQIEFFGRMDQQVKIRGHRIEPGEVESALLSHNSVQDAAVVICA PADQDSGAEMVAFVAARNTEDEDTQEEEAVDQVQGWETHFETAAYSEVKDIRQSEVGN LADLAASIQRESAPHEPIPQRPYTGPAEQSFAQGRLWFLDQLNLGATWYLMPLAIRIR DLPRPSILSGRAGSVDVTIEGSVYGALQSFCRTRSVTTFVVLLTVFRIAHFRLTAVDD PFERIVSALVPGSRNTSRNPLVQLMFAVQSVEDYDQVRLEGLESVMMPGEASTRFDME RQMIYELEANEEELLTDPAFFTSLRTRLGEKIKHVEILPKTMKATNELSKYRYAAVLH ROWSONGALDAIFHHFEPPKEGARTLIEFPTDYEGRNVNTLTNRPLNSIQSRRLGTQI GQLRVAALSAALFALERRHETLRTTFEESDGVGVQIVGEARNSDLRVHDVSTGDDGEY **ATIGTPIANRNRPELETLVGCFVNTQCMRISIADDDNFEGLVRQVRNVATAAYANQDV** 

AWLHERHWPAESLVGVLSPRSCETTIAYEGIMKANLAYLPLDVYAPDARLAAILDTVE
GERLLLLGGGVPQPGIQIPRLSTAYIAEALSHATTVDVTSIPQPSATSLAYVIFTSGS
TGKRGVWLEHENGTYRLWINVINVIPPESGSALLPWBAARAMDAAMBLYAFBLTYARLINGG
TTVVCIDBDTMLDIAALNSTERKEWNRAAFFTPAFILKQCLAFTPELVANLEILHTAGDR
LDPGDANLAGKTARGGIFNVLGHTENTAYSTFYPVVGEETFVNGVPGRGISNSHAYI
IDRHQKLVPARGYWGELILTCDGVARGYTDSALNCDRFYYIDINGKSTWSTRTGDKARY
PREGGLEFFGRMDQMYKIRGVRIEGEVENTLLDHKSVLAATVVRRPPNGDFEMIA
FITIDAEDDVQTHKAITYRHLGGILPAYMIPSTYTOPVGETFCOLGGRANY
VQKRRSTAARVPPRDEVEAVLCEEYSNLLEVEGYBLTTGFPDGGSLLATKLAARLSR
OLNTRVSVVKDVFDQPILADADIIRRGSHRUDPIPATTGFVPGSFRAGRAPHTEBL
NGASWYLWDYRDEALDIIRRGPLGTKALAVALINLHRREALTTFEDHGGVGVQVJQPKSS
OLLRIDLSDAVDDTAXLAALKREQTTAFDLTSEPGWAVVDLLTDECRTHQYTSFSU
NGASWYLWTKOELGGFYSAAIRGOEDESGARSLETTFEDYRORDEWOSTGREGESL
OLOWNYROBICADSTREELTDLERPSILLSGEADAVPWYLDGFGTYVQLLTDECRTHQYTSFSU
LLAAFRTAHYRLTGTLDATVGTPIANRNRPELEGLIGFFVNTGCMRWAISETFESL
VQQVKLTTFAFARNQDVPFEQIVSTLLPGGSRDTSRRELOVWRFLQSODGHTQDEG
SSTLTYAALDGGSWKLAHRLCGRNWAPFETLAYRFSTRUDFCRTHQYTSFSU
MYDGALETPLSTRLDLEVHLFGGENGSSILLSGEADAYPRTGFYVGTGLASSSGGDHGU
HSGRPTATSLAYWHTSGSTGKRCWIDHRSIIRLWKNSDVVATLEPPVRANNVSN
MYDGALATSTRUGGTLVCLOYLTLLDSKILTNVFREDYOVARALGYBUDYN
APARIEDISTRUGGTLVCLOYLTLLDSKILTNVFREQOVNAARFTPVLLKQCLGN
MPAIISRLSAVWHTSGSTGKRCWNIDHRSIIRLWKNSDVVATLEPPVRANNVSN
NGVPIGRSTTNGGTLVCLOYLTLLDSKILTNVFVEQOVNAARFTPVLLKOCLGN
MPAIISRLSAVWHTSTTSGSTGKRCWNIDHRSIIRLWKNSDVVATLEPPVRANNVSN
DANVLRKRANDEPEMIAATTGYGDDETTEWBESKYVTGOGGLABSTROHTLSNLC
XVGGLGWTSTRUGGTLYGATTGTTSQDEGARGYTVTGOGLARGYTPVTGOFLVY
TDGEENIKAYTGGREYNTRPKDFEIEFFGRMOQVKITGHFLSNLC
XVGGLGWTSTRUGGSTWCKEWLDETTSALLDNRFPCHILLETGAGTGMILSNLC
XVGGLGWTSTRUGGSTWCKEWLDETTSALLDNRFPCHILLETGAGTGMILSNLC
XVGGLGWTSTRUGGTLOVDPAFVSUKRYFFGINRATARDFLANTGAGTGMILSNLA
XVGGLGWTSTRUGGSTWCKANTVFORDYN
XVGGREFFTORTEGTERFEENLLVURGTLONDFFYVRYNGYFOUNTNYNGY

21375 21255 21376 TTGTCAACAAGTCACTGAGCGAGGATGATATGGAGGAAGGCCAGAACTCACTGGACGGAT 21435 21495 ä; 120 240 300 9 181 TCGACTTTCAAGCGAATCAATTGAACCAGAAGTCACTGGGTGACCTTCTCAAGTCTTCAG CAGCTTGGGTTGCCGGATGGCCGCTCAAAGCTGCCCATCGATGGCAATGG AACCTGCTTTCTTCACCTCGTTGAAAGACAGGTTTCCAGGTCTGGTGGAACATGTTGAGA ACCCTGCATTCTTTACATCTTTGCGTACGCGCTTGGGTGAGAAGATCAAGCACGTCGAAA TCCTGCCAAAGAACATGGAAGCTGTGAATGAGCTCAGTGCGTATCGATATGCCGCTGTTG 121 TGCACGTTCGGGGTTCACTTGGAGATGAGCTTGTGCTTCCGGTTGAGAAGATGACTGGA 241 ATGCTGCTATCATGCCAGTCAGCAAAATTCCTTTCGAAATCACGGCCTTTGAAAGACAGG -----GCTATCAACCATTCGGTCCAGCGCCGAGGGCGACTCATCACTATCCGTTCCCG ACATCTTTCGCATTGCTGGGGAAGCCGGGTTCCGTGTCGAGGTCAGTTCTGCACGACAGT 42; Gaps Length 46899; TCGTCGCTTCCCTCAATAGCAACATCGATGAGTGGCA------;--Indels Score 240.2; DB 8; Pred. No. 7.5e-62; 0; Mismatches 418; 24.0%; 55.0%; Conservative Similarity 563; Query Match Best Local S. Matches 563 21076 21136 21316 21436 61 301 338 391 g ò qq οŽ q ŏ qq δy . අු δy qq δy δ q δλ 21615

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NSVIKSVPSLAGKAEVHIGTAQDISOLSDLAPDLVVINSVÄOYFPSPEYLAQVADTLV
HLPGVKRLFFGDMRTNATNKHFLAARAVRTLGDNATKDSVRQKMAELEEREEELLVEP
AFFTALQDRFPDLVHHVEILEKNMHATNELSAYRYAAVVHTRHHDSVPVHTIEKGAMV
ISTASSANDRNELLQFLRKSKSSAVALSNIPPRATKVERQIVESLEEBEKSKLDGAAW
ISTIRSEADSRASLSVPDLHELAQDAGFRLEVSAARQWSQSGALDAVFHHLPSPSDTR
RTLIKFPTDNHLRSSATLANRPLQGLQFRRRAALQVRERLQSLLPTYMIP"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                  Length 1497;
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                                                                                                                         Score 203.2; DB 8;
Pred. No. 1.2e-50;
.....tches 233;
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A36771
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61.1%;
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KVEWQEWLDDTIKTLRDGQAPGHVLEVGTGSGMILFNLGDGLQSYRGLEPSKSAAAFT
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Submitted (07-SEP-2001) Zocher R., Fakultaet II,
Institut, Franklinstr. 29, 10587 Berlin, GFRMANY
orf based on homology with 218755 and 248743.
Location/Qualifiers
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/strain="ATCC 74289"
/db_xref="taxon:100904"
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/protein_id="CAC69934.1"
/db_xref="GI:15626355"
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Leitner, E., Schneider, E., Schoergendorfer, K. and Weber, G. Cyclosporin synthetase
Patent: US 5827706-A 4 27-0CT-1998;
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Pred. No. 2.3e-46;
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/db_xref="taxon:40622"
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                  Schoergendorfer, K.
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0; Mismatches 258;
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Leitner, E., Schneider, E., Schoergendou Cylosporin synthetase
Patent: EP 0578616-A 4 12-JAN-1994;
SANDOZ LTD (CH)
Other publication JP 6225773 940816
Other publication AT 140392 940515
Other publication AT 398578 941227
Other publication AT 398578 941227
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VISGRPEDIEGIEGDWYGLFINTIPIRLHGSKTPFLQLYKDWOKDRLAEAYSTHPLYE
IQSRSAVKQGLIDHILVFERANSTYPELQLYKDWOKDRLEAYSTHLYE
IQSRSAVKQGLIDHILVFERANSTYDRSQVDSDLFQIHNFTVADETNYSFYLM
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YILNDCGCSHVVSQAHFAPLLETGLNVIYMEDIQIEDGSCLHSVNSADDLLYHITTSG
TYTKKRQVQYGFHRNMANLLAGPETRSGIDFENDVLQFATPAFDKTYGGT
LHIYPERAIKROVYQLAFAFKEHQTTSSYSPTAFIKMIFSEQEFANAPPHDVKHLITAG
EQLIVSSLLQDVLRQRSMYLHNHYGPSETHVVSAYTHPGNOIPEFPRIGKFIDTDCTDL
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AYYCSHARLDSSALROYLANKLPEYMPAKWWWDSIPLTPROKKUDGSALPKPEASIS
SNYTAAPRILLEVKLSQLEPOVLKEAPIGIHDNFFDRGGHSLKATVLVSRIAKEFHVO
VPLKDVFAHPTVEGLALJIRHARKNPFASVAQAKEQFTYPVSSAQKRYYLORILBNGG
VGYNMPAVLELEGKLDJREKLAAVFKELISRHEPLRTSFVPGEDAEPVQRIHREVPFTL
SEASSAAGFWRPDLSQAPKKALNKALNEMHLILVDWHHTISDGVYGULIREFTE
RYANRILKPLRIQYRYAVWQCBFKGDTYKKQETWHLAGGSGELPYLELPFDKRRPA
RRNFTGGKVLFQMNEDITSRLKARAPNRQAPTGRTWELPFDKRRPA
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/db_xref="G1:2522212"
/db_xref="G1:2522212"
/translation="MTRANSIQDIYPLSYMQEGLLFHSLLQKDSRSYVEGASFTIEGE
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AFVERIREKDRAKGFHLQKDMLARITLIRGKOYTCIWTFHHIMMGWCLGILVLKEF
LQ1YASKIKGAPLSLEPVQPYGTYINWLMEQDKEKAVSYWDNYLSGIEQQTLLPKQKK
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FenA (fenA) gene, complete
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Hsieh,J., Lin,G. and Liu,S.
Analysis of the Fengycin synthetase Gene fenA
Thesis (1997) Microbiology and Immunology, Chang-Gung University
2 (bases 1 to 10513)
Hsieh,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-SEP-1997) Microbiology and Immunology, Chang-Gung University, 259 Wen-Hwa 1st Road, Kwei-San, Taoyuan 333, Taiwan R.O.C
                                                            GCTCATTTCTCGTATCGACCAACGACTCAAGGTCCGTATCACTGTCAAGGATGTCTTTGA
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SVRAYRTGDBARYRRKDGQIEFFGRWDQQIKIRGHALELABYEHAMLHHDAVRDAVVV
IRLQGDQEPEHIGFVVVRANDETVQQDLSRTHGAVNSANWEEQFEIQTEKEIRNRLQNL
LPSYWYPARITILLDQAMLDANGKYDRKDLARRAQTVSKAEKLESARVAFRNEVSVVLC
EEFSDVLGVEVGVBOSFFDLGGHSLMATKLAARISRRLAARVSVKEVFFDDALAI
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Sordariales; Chaetosphaeriaceae; mitosporic Chaetosphaeriaceae;
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Unpublished
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/note="SDZ 214-103"
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Strain="NRKL 18230"
/db_xref="texn;72418"
/clone_lib="pCB11"
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/protein_id="CAA65395.1"
/db_xref="G1:1770180"
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oligospermum gene encoding synthetase
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5900 GAAGGTTTGGCGTCTGTCATCAGCGAAGGAACGG 5933

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BASE COUNT 3016 a 2429 c 2550 g 2518 t
ORIGIN

Query Match 7.2%; Score 71.6; DB 1; Length 10513;
Best Local Similarity 52.8%; Pred. No. 3e-10;
Matches 208; Conservative 0; Mismatches 174; Indels 12; Gaps

5669 ------GCTCCTGACGGAGCGCAGATCGGGAAAACCTACACAGCGCCGAGAAATCTGA 5720 5779 GAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGTT 662 902 5552 GAAGTGCGCAAGCAGCTTGACACTTTGCTTCCGGGCTACATGATCCCTGCTCATATCATT 5721 CAGAGATGAACCTTTCCCAGCTGTG-GGAGGAAGTGCTGAAAAGCGGCCCTGTCGGCATT 843 ACCGATCACTTCTTCAATCTCGGTGGACACTCTCTTGGCCACGAAGCTCATTTCTCGT 723 AGGGCAAAGGTTGTACCGAAGCAGCAGCAGCAGCGCCGTTACCGACATTTCCCATCAGT 783 GAGGTCGAAGTCATTCTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATT 603 ò q ŏ g ŏ g ò g ò a

SIWNGYGPTENTTFSTCFHIEKLYEHSIPIGRPIGNSTAFILNKWGMLQPIGAVGELC VGGDGVARGYLGRPDLTKEKFVPNPFAPGEQMYRTGDLARWLPDGTIEYVGRVDDQVK

5899

962

Oy Db

GCGGATCTAGCATCTGTCATCCGTCAAGGGCTGG 996

963

LHIYQALGEGRLPYLQPYQPYGTYIKWIMQODREEAAAYWKRRLQHFEKASSLDRRNE
VSGSELGOVOTPTISBRETSDLQKIAAASGATUTUTVODALWGUTLLQKRNECDDAVTGS
VVSGSELGOVOTPTISBRETSDLQKIAAASGATUTVTVODALWGUTLLQKRNECDDAVTGS
VVSGRDSELEDVENIVUGLFIYDFRVQSRLLSFSGLVSRMQKEMTBAEAYSYFPLYD
IQAQSALKQELIDHIIVFENVPTQQEIBGLNQTGSFGFSVENFAMEETNYGGSVKVI
DRACETLEVRINTHTGLYBERIATIATIATUGANSALAPTATAARTAA
AEYNTTGAVSALAPTHGLFERQVAITPDRTALRFSGGSLTYAQLDAYANRLAARLTA
HGITKESIVGVLSERSPDMLTAVLAVLKAGGAYVPLDPAYPEERLSYMLKDSGAALLL
TOGLKARPYSGKTLEVDMTAALNEBESCHSHAGADSDSLAYVIYTSGSTGRRKGVAV
ENRQAVSELTGAWQMPELEEDDIIMKKTSFSPDASVWQLFWWTLSGSSARTLRCGAY
FERQAVSELTGAWQMPELEEDDIIMKKTSFSPDASVWQLFWWTLSGSSARTLRCGAY
DALAMYKAIREECVTTAHFIPAMLNSFLDQAEIBAPRSLKRVPAGGEPLAPHTAARFR AF023465

AF023465

Bacillus subtilis fengycin synthetase FenE (fenE) gene, complete /translation="MPQQPEIQDIYPLSFMQEGMLFHSLYDEGSRAYFEQASFTINGQ LDLDRFQKSMDAVFDRYEIFRTTFIYKNVAKPRQVVLKNRSCHVHFEDISHLNEREKE HCTEAFKEQDKKRGFDLQSDVLMRISVLKWAPERYVCIWSHHHILMDGMCLGIIIKDF LPALHIQYKDYAVWQEAFKKGETYKTQEAYWLKQLEGELPVLDLPADYARPPVRTFAG DQVSFTLDQELTAGLHKLARENGSTLYWVLLAAYTALLARLSGQEDIIVGSPIAGRPH KDLEPILGMFVNTLALRARPEGGKPFAQFLQEVRETALEAYEHQDYPFEELVDKLGMT RDMSRNPLFDVMFVLQNMDQESMQLKDLCLRPATNVEHQVSKFDLTLYAYEEANGSMM FQMEYSTDLYQKNTIEMWLHYLMNMLRAIIQDSEAALGTIHVLDENETHFLIHELNCT KREYPRHETISRLFELQAAQTPDAIAVAGDEQTLTYKELNIRANRIAAVLRRKGVGPE TVVALLTTRTPEIAAGMLGILKAGGAYLPIAKDLPADRISYMLSDSGAKILLQSEKAN NQRLDLELKCEKIVIEE1QGQGETKNFEAPAGPHSLAY11YTSGSTGKPKGVM1EQRS VIRLVKNSNYIEFTPEDRLLLTSSLGFDVVTFEILGPLLNGAALHLTDKETFLDSHQL KRYIEQNGITTMWLTASLFNHLTEQNEKIFSRLINLIIGGEALSASHVNRIKQACPEL Chen I., Lin,G., Shu,H. and Liu,S. Analysis of the Fengycin Synthetase Gene fenE Thesis (1997) Microbiology and Immunology, Chang-Gung University Direct Submission Submitted (06-SEP-1997) Microbiology and Immunology, Chang-Gung University, 259 Wen-Hwa 1st Road, Kwei-San, Taoyuan 333, Taiwan, Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. 1 (bases 1 to 7681) /product="fengycin synthetase FenE" /organism="Bacillus subtilis" /strain="F29-3" /protein\_id="AABB0956.1" /db\_xref="GI:2522214" /db\_xref="taxon:1423" Location/Qualifiers /codon\_start=1 /transl\_table=11 AF023465 AF023465.1 GI:2522213 /gene="fenE" /gene="fenE" /gene="fenE" (bases 1 to 7681) Bacillus subtilis. Bacillus subtilis .7681 .7681 Chen, ] ACCESSION VERSION KEYWORDS SOURCE ORGANISM source DEFINITION REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE JOURNAL gene RESULT 13 AF023465 LOCUS RBS CDS FEATURES

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AFU87452 8371 bp DNA linear BCT 23-SEP-1998
Bacillus subtilis peptide synthetase (fenC) gene, complete cds.
AF087452
                                                                                         SINLQQGPLLHAAWFKŢLSGDYLFLTHHLVVDGVSWRILLEDLSAAVHQAASGQAIQ
LPPKTDSYQEYARRVQDYAQSSKLIREETYWRSVEEEKAAELPYEMPYMENMNSSERE
TLRFSLTEADTAVLLQKVNHAYGTDYQDILLTAASLALCOMTGGSKLENAMEGHGREH
ILPDLDISRYGWFTSIYVAUFTOFPQADELCPAVKTVKDTWGTRIGRIPNKGVGYGMLKYL
TPPEHKSNYFSKTPRIGYPLOFPONDESQDBRPSGLGSGRDITPTWKREQLIEMSA
MAAENQLHFQLSYPPARFHRGAMERLITMIECYLQDIMKHCAEKQNTEKTLEDSSSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3040
                                                      TERVIDQGSVQGAVPWTPIQHWFLSQDIKERHHFNQSVMLFSPDCLSENALRASLKKL.
AEHHDALRMIYREDSGQQMQINQDIHESKLYSLRISDLSDSGMDWETSIKEEVANLQQ
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IRGYRVELGEIESALRHIDGVKEAAVLARTGQLGTKELYAYISVKEGTDAEQVRTHLS
              QMLPGYMMPAYVIEMDALPLTANGKLNRKALPEPDITSKQTYVPPRNDLEEQLAIIWQ
EVLGTQRIGIEDSFFELGGDSIKALQVSARLGRYGWSLHASDLFRHPKIKDLSAVIRK
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                                                                                                                                                                                                                                                                                                                                                                            603 GAAGTCCGCGAGAGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 GITCTGGACAAGAIGCCTCTCAACGCCAAIGGIAAAGIIGACCGGAAGGAACICTCTCGC
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 8371)
                                                                                                                                                                                                                                                                                              Length 7681;
                                                                                                                                                                                                                                                                                              Score 66.8; DB 1; Length 7 Pred. No. 8.7e-09; 0; Mismatches 177; Indels
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/strain="F29-3"
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1749 c 1971
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sal Similarity 52.0%;
205; Conservative
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Best Local Similarity
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AUTHORS
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AF087452
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TSLVHGYGPTEATVDAAFYACDPELDKDRLRLPIGKPVPGARLYVLDPHLAVQPVGVA
GELYTAGAGYARGYLMRPELTEERFLDDPFYPGERMYKTGDLAHWLPDGQVBFLGRLD
DQVKIRGYRIEPGECEAALRSIEGVHADAVTVRTESGEAELCAYAEGLGRNEVRKQLE
TLLPGYMIPHIIELEGWPYTPSGKLDRRALPAPDGAADRETYTAPRNLTEMKLSQUL
EEVLKSGPVGIHDNFFDRGGNSLKATALVSRIAKEFGVQVPLKDVFAHPTVEGLASVI
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ILGMEVNTLALRTREBECKRPTQFLQEVGEVALEAYEHQDYPFEBLVDKLGYTRÐMSR
NPVEDAMFILLIGNBUKQDIHLGDIKARPANVIHQISVEDMTLMAAESDGVIKCDMEFST
DYPRHYTIERWITGHFELRARTSHPYTTLSQVDILSEKEKGKILIELNKTHVECSQT
DTVFHRMFEKRAEETPEHIAVIDGEKQISYRHLNEKANRLARTLQEKGKETQPIVAVL
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KAPPESGYTLEVDMYSLANDESERYBLHQABSDSLAYVIYTSGSTGQFKGYAVBHLQA
VSELTGMONGPPLEBDIINMKTSESPSWQLFWATLSGASALLLFSGWERDPALM
VKAIREEGVTTAHFIPAMLNSFLDQAEIEAPRSLKRVFAGGEPLAPHTAARFASLLPE
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DIGDISRVCLDDESFYESKKMHLSSSPAPEDSAYIIYTSGTTGAPKGVIVTHRNFAHA
VLAWRRIYQLDQMPVRLLQMASFSFDVFSGDLARTLANGGTLVICPDETRLEPAELYA
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KRRLINSYGYTEATIDSSYYENNMGEBYSGDSYPIGIPENNYKLCVLSGYDQIQPIGI
AGELCIAGAGVAKGYHETEMEKFRENPRFYPGERLYRTGDLACWLDNGTLRLLGRI
DHQVKINGYR EFPEEESVLLOTGLVNRAVVANQUNDTNOQARLAAYILPSDADTTALR
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LRKLTEHHDAVRMVFTQDHTGRVVQYNRGIQITENELFGFHLTDWTKEQAKGTLLKEK
FAAEEIVLQSNMNVKEGPLLQAGLFKTREGDHLLITIHHLAVDGVSWRILLEDLAAAY
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SDRHQSSAETAAFVLASDWTKKLLFETQQAYGTDANELLLTALGMALYEWSGHEQIVI
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RTRAVSPVSSTLHGLFERQAALTPDRTALRFSGGSLTYAQLDMYANRLARLTAHGITK
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IQYKDYAVWREGFKKGDTYKTQEAYWLKQLEGELPVLDLPADYARPPVRSFAGDQVSF
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QIWEDVLSVSRVGIHDSFFELGGDSIKALQVSARLAAEGWSMTISDLFRYPTVHELSG
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ELVINALITDGRLQVKAVYTRVFHENTIQCLMDSFHSHLIEIIDDCTKKKEREKTLSD
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GNRGSKAEKDMLGMFVSSLPIRKTVDSDADFLSFARSVGREQLSVMRHQRFPYNLLVN
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52.0%; Pred. No. 8.8e-09;
tive 0; Mismatches 177; Indels
                                                                                                                                                                                                                                    /product="peptide synthetase"
/protein_id="AAC36721.1"
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clone_lib="pF6A5"
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                                                        /gene="fenc"
692, 8371
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B subtilis genes for peptide synthetase and penicillin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 39822)
Tognoni,A., Franchi,E., Magistrelli,C., Colombo,E., Cosmina,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
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/db_xref="GI:509460"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (24-JAN-1997) F. de Ferra, Eniricerche S.P.A.,
Submitted (24-JAN-1997) F. de Ferra, Eniricerche S.P.A.,
Environmental Biotechnology Laboratories, Via F. Maritano, 26, S.Donato Milanese (MI), ITALY, 20097
Revised by author 27-JAN-1997
On Jan 29, 1997 this sequence version replaced gi:509465.
Location/Qualifiers
                                     783 GAGGTCGAAGTCATTCTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATT
                                                                             3582 CAGAGATGAAGCTTTCCCAGCTGTG-GGAGGAAGTGCTGAAAAGCGGCCCTGTCGGCATT
                                                                                                                      843 ACCGATCACTTCTTCAATCTCGGTGGACACTCTCTTGGCCACGAAGCTCATTTCTCGT
                                                                                                                                               ATCGACCAACGACTCAAGGTCCGTATCACTGTCAAGGATGTCTTTGACCATCCTGTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JUN-1994) Grandi G., Eniricerche S.P.A., Genetic Engineering and Microbiology, Via F. Maritano, 26, S. Donato Milanese (MI), ITALY, 20097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A putative new peptide synthase operon in Bacillus subtilis:
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234883.1 GI:1805667
genicillin binding protein; peptide-synthetase; pps operon.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                         963 GCGGATCTAGCATCTGTCATCCGTCAAGGGCTGG 996
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    .39822
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/label=CDS1
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Direct Submission
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YALDLFKQSLKKQGITVKGDIKTGEAPSSSDVLLSHRSMPLSKLFVPFWKLSNNGHAE
VYKEMGKYKGEGSWEKCLBVLNSTPLPEFGVDSKSLYLKDGSGISHIDAVSSDOLSQ
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                                                                                                                                                                                                                                                                                                                                                            HDDMRLSPDMPWSDEYTYYGAPISALTASPNEDYDAGTVIVEVTPNQKEGEEPAVSVS
                                                                                                                                                                                                                                                                                                               TEVRTDGTLKGKKLNGNLYLKGKGDPTLLPSDFDKMAEILKHSGVKVIKGNL1GDDTW
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RNEQKDLHNLIGISMQYQPLQWHNADDFDYETALYFSGYTANELSVQIQERIDNGTIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="Swiss-proT:P39845"
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LQRLLPGYMVPAYMIEMEQWPVTPSGKLDRNALPAPGGAADAETYTAPRNVTEMKLSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIIKSQRITVMESTPALIIPVMEYVYRNQFKLPDLDILILGSDMVKAQDFKTLTDRFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAGELCIGGAGVAKGYHHKPDLTQMKFTENPFVSGERLYRTGDRACWLPNGTIRLLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDYQVKINGYRIETEEIESVLLQTGLVREAAVAVQHDKNGQAGLAAYIVPSDVNTNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLAAEETVIQSKMNVEKGPLLQAGLFKTAEGDHLLIALHHLVIDGVSWRILLEDLAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPESEMSHIFLDDEGSFEESNCNLNLSPAPEEPVYIIYTSGTTGAPKGVIVTYQNFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHITPLASQADQGPAEGEAELTPIQRRFFGQVHAFHYHYNQSVMLFSEKGFNANALHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEGALNHSISRNDAIRFQLLEGEELEPRLHLTEYKYYPLRIIDFSNVEN
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RBS gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPQQPEIQDIYPLSFMQEGMLFHSLYDEQSRAYFEQASFTHGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IETFIKPEYLSSGPLFRACVITMGNNRGFLLLDMHHIIADGVSMSTLVOBFTDLYCGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADYTGHILYIDECENNSIPADVNIEEIVTDQPAYVIYTSGTTGQPKGVIVEHRNVISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKKERVTVLNQTPTAFYGLMLEDQNHTDHLNIRYVIFGGEALQPGLLQSWNEKYPHTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIWEELLINVDELGVSANFFKLGGDSIKALQVCARLKQRGFETTVREMFEHQTLGELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVRKDVRAIDQGPVEGEITWTPIQOWFFSQSLESHHFNQSVMIYRAERFDEAALRKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSLVTHHDALRIVCRHEDGRQVQINRGIDLSDEELYALELFDVKDSLTEARNTIEEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRMQEHIRLETGPLLHAGLFRTENGDHLFLTIHHLVVDAVSWRILFEDFSTAYKQAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHIYQALGKGQLPDLPPVQPYGTYIKWLMQQDREEAAEYWKKRLQHFEKSTPLPKRTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRRTADGNYKADQVSFSLAPDMVEKLTEAAQNWGVTLNTLFMSIWGVLLHRYNAADDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEQQVIQLFNETERPYVNKTIPQLFEEQAHKTPEAAALKMGNECWTYROLOVRANOIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HALIEKGVGSGDIVAVMMGRSMEMPAALLGIWKAGGAYMPLDPHFPAERLSFLLKDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGELCISGAGLARGYYKQQELTQKAFSDHPFLEGERLYRTGDAGRFLPDGTIEYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFDDQVK I RGY R I ELREI ETVLRQAPGVKEAAVLARDVSAEEKELVAY I VPEKGNSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HADLERVIGMEVNTLAMRSKPEGHKTFSSYLHDIRHLALTAVEHQDYPFEELADKLDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFEYSTALFEEETITQWASYFIELVKGVTADTEMRISNMQLLPAAERRLLLEKMGQYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGLMLDRSPDMIIGVLSILKAGGAYLPIDPEYPKERISFMLNDSGAKLLLTERGLNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLKNALPDFMLPARMIQIDSIPVTVNGKLDQKALPEPEKQAYTADDISPRNEIETVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRESYLEDIDISRTVGWFTSIYPVWLDMRDSDHKDKEERLGHLIKQTKDMLHRIPHKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aldisgavssgclnmhiiynrfqfeektiqtfsrhfkqtleniiehctgkenqewsas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFGSVISGRPSAIDGIESMVGLFINTVPVRIRSAEGITFSSLVKAVQEDILSSEQHGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GESIKLPQKTDSYLTYSQRIADYSISRQVQREAAYWDECENRHIQPIPKDNDAASNTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDTEVIDFELSRHHTELLLTAAHKAYSTEMNDILLTALGLALQKWTGNNQFKISMEGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNQIICPSAELANEYGPTENSVATTILRHLNKKERITIGHPIRNTKVFVLHGNQMQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYPRNENIVSLFEKQVAQYPEHIAVVCGHSQLTYRDLNEKAERAAAMLIKQGVRTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agygvlkyiskrwgsoknspeisfnylgofdodiosnafevsdikpgneispnwerpy
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RBS gene CDS

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                                                                                                                                                                                 894 ATTTCTCGTATCGACCAACGACTCAAGGTCCGTATCACTGTCAAGGATGTCTTTGACCAT 953
                                                                                .;
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                                                                                                                                                                                                                                               954 CCTGTATTTGCGGATCTAGCATCTGTCATCCGTCAAGGGCTGG 996
                                               Score 59; DB 1; I
Pred. No. 2.5e-06;
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le: 2767 secs
                                              5.9%;
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Best Local Similarity
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48 4.8 18660 21 46.8 4.7 6465 24 45.4 4.7 8268 24 45.4 4.5 4615 22	45.4 4.5 34071 22 AAF90033 45.4 4.5 42717 22 AAF90032	42.8 4.3 88421 24 AAL40781 42 4.2 2365589 24 ABA90521 41.8 4.2 58857 21 AAAS8471 40.4 4.0 7347 23 AAS54136	39.8 4.0 3798 24 ABK74884 39.8 4.0 3798 24 ABK74902 39.8 4.0 5451 22 AAF76319 39.4 3.9 68750 21 AAZ55887	39.4 3.9 71989 21 AAA29349 39.2 3.9 1172 20 AAV69527 39.2 3.9 4620 22 AAF26318	27 38.8 3.9 1178 20 AAV69562 28 38.4 3.8 31122 14 AAQ40706 20 37 0 2 0 2040 2) XARD-5706	37.6 3.8 4403765 22 AA199683	32 37.4 3.7 2301 22 AAH52513 S. epidermidis	37.4 3.7 2634 22 AAH34823 S. epidernidis 37.4 3.7 3321 22 AAH54694 S. epidermidis 37.4 3.7 3602 22 AAH54666 S. epidermidis 37.4 3.7 3602 22 AAH54666 S. epidermidis	39 37.4 3.7 5968 22 AAH5445 39 37.4 3.7 6968 22 AAH52683 40 36.8 3.7 1716 22 AAF26315		ALIGNMENTS	RESULT 1 AAA58762 ID AAA58762 standard; DNA; 11212 BP.	XX AC AAA58762;	XX DT 20-OCT-2000 (first entry) XX	DNA encoding a cyclohexadepsipeptide synthetase.	<pre>KW Cyclohexadepsipeptide synthetase; filamentous fungal cell;     Kw cyclohexadepsipeptide; antibiotic; ss.     xx</pre>	OS Fusarium venenatum. XX FH Key Location/Qualifiers FT CDS 2709559		XX PN WO200042203-A2.	XX	Pr 13-JAN-2000; 2000WO-US00913.	AA PR 13-JAN-1999; 99US-0229862. XX	PA (NOVO ) NOVO NORDISK BIOTECH INC.	PI Berka RM, Rey MW, Yoder WT;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compug	eic search, using sw model	June 4, 2003, 17:28:42 ; Search time (without a 8302.948 M	US-09-482-788-1_COPY_7000_8000 1001 1 aacctgctttcttcacctcgtcc	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	2185239 seqs, 1125999159 residues	hits satisfying chosen parameters:	length: 0 length: 200000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	ان عا	<ul> <li>/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*</li> <li>/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*</li> <li>/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*</li> <li>/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*</li> <li>/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*</li> <li>/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*</li> <li>/SIDSZ/gcgdata/qeneseq/geneseqn-embl/NA1986.DAT:*</li> </ul>	: /SIDS2/gcgdata/geneseq/geneseqn  : /SIDS2/gcgdata/geneseq/geneseqn  0: /SIDS2/gcgdata/geneseq/geneseq	2: /SIDS2/gcgdata/geneseq/geneseg/3: /SIDS2/gcgdata/geneseq/geneseg/3: /SIDS2/gcgdata/geneseg/geneseg/4: /SIDS2/gcgdata/geneseg/geneseg/	5: /SIDS2/gcgdata/geneseg/geneseg6: /SIDS2/gcgdata/geneseg/geneseg	./: /SIDSZ/gcgdata/geneseq/geneseg .8: /SIDSZ/gcgdata/geneseq/geneseg .9: /SIDSZ/gcgdata/geneseg/geneseg	10: /SIDS2/gcgdata/geneseg/geneseg 11: /SIDS2/gcgdata/geneseg/geneseg	2: /SIDS2/ 3: /SIDS2/ 4: /SIDS2/	s the numbe er than or ved by anal	SUMMARIES	& Query Match Length DR ID	11212 21	.2 9633 22 .0 46899 15	18.7 1713 15 AAQ54389 5.3 13029 23 AAS51470	.0 41599 22 .0 1200 20	7178 21
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                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                      The present sequence encodes a cyclohexadepsipeptide synthetase polypeptide. The specification describes a method for producing heterologous polypeptide. The method comprises cultivating a mutant of a parent filamentous fungal cell, which produces less cyclohexadepsipeptide than the parent filamentous fungal cell which produces less cyclohexadepsipeptide than the parent filamentous fungal cell when production of biologically active compounds e.g. antibiotics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes an enzyme which has cyclosporin synthetase-
like activity. This sequence was isolated from Tolypocladium niveum
(formerly known as T. inflatum GAMS). The enzyme encoded by this
sequence catalyses the peptide biosynthesis of cyclosporins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structurally related molecules. This sequence may be used for the production of cyclosporin by transforming a vector containing this sequence in to a recombinant host. This allows effective production of antibiotic cyclosporin or its derivatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                        Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum;
T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase; ss.
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SANDOZ PATENT GMBH.
SANDOZ-ERFINDUNGEN VERW GES
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93CH-0001375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                gene from T. vasinfecta. This fragment was isolated using primers derived from the Tolypocladium niveum (formerly known as T. inflatum GAMS) exclosporin synthetase gene, corresponding to bases 40309-40328 and 42018-41999. The T. niveum gene encodes an enzyme which catalyses the peptide biosynthesis of cyclosporins and structurally related molecules. The T. niveum sequence may be used for the production of cyclosporin by transforming a vector containing the gene sequence in to a recombinant host. This allows effective production of antibiotic cyclosporin or its derivatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTATCAACCATTCGGTCCAGCGCCGAGGGCGACTCATCATCATTCCGTTCCCGACATCTT
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                                                                                                                                                                                                                                                                                                                                                                   - which codes for enzyme having cyclosporin
                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a fragment of the cyclosporin synthetase
                               .yme; cyclosporin; synthetase-like activity; Tolypocladium niv
inflatum GAMS; biosynthesis; vector; cyclosporin synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 18.7%; Score 187.6; DB 15; Length al Similarity 59.3%; Pred. No. 7.6e-50; 395; Conservative 0; Mismatches 259; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1713 BP; 390 A; 490 C; 469 G; 364 T; 0 other;

    T. vasinfecta cyclosporin synthetase gene fragment.

                                                                                                                                                                                                                                                                                                              Schoergendorfer K,
                                                                                                                                                                                                                                                  (SANO ) SANDOZ LTD.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH
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                                                                                                                                                                                                93AT-0000437.
93CH-0001310.
93CH-0001375.
                                                                                                                                                                                   92AT-0001403
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                                                                                                                                                                                                                                                                                                              Schneider E,
                                                                        Tolypocladium vasinfecta
                                                                                                                                                                                                                                                                                                                                                                  Isolated DNA sequence - v
synthetase like activity
                                                                                                                                                                                                                                                                                                                                        WPI; 1994-010432/02.
                                                                                                                                                         05-JUL-1993;
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                           21196 TACATGTGCGTGGCTCGAGAACAATCAACTATACACCAAGTCTCTCCCAACGCCTGGA
                                                     TCGACTTTCAAGCGAATCAATTGAACCAGAAGTCACTGGGTGACCTTCTCAAGTCTTCAG
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to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
for antibiotic development. The antisense nucleic acids can also be used
                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                          Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 4-17; 18pp; Japanese.
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                                                                                                                                                                                                                     Local Similarity 51.9 es 150; Conservative
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1532 CGGCCATTCGCTGCTGGCCACGAAACTGAGCGCACGTCTAAGTCGCAGACTGGACGCCGG 1591
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                                                                  412 CCGCAAGCACGTTGGACTTTGTGGCGCGCACGCACGGAAATCGAGGTCGGTTCTCTGCGA 1471
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                                                                                                                                                    TGGACACTCTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTCAAGGTCCG
                                                                                                             TATCACTGTCAAGGATGTCTTTGACCATCCTGTATTTGCGGATCTAGCATCTGTCATCAG
                                        CAGACAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTC-ATTCTTTGCGA
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                                                                                                                                                                                                                                                                                                                                                            AAS51470 standard; DNA; 13029
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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27-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene encoding Iturin A for the production of large amounts of Iturin
                                                                                                                                                                           613 AGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGTTGTTCTGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                733 TTGTACCGAAGCAGCAGACAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAG
                                                                                                                                                                                                                                                                                               793 TCATTCTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACT
                                                                                                                    Gaps
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Sequence 13029 BP; 1978 A; 4677 C; 4485 G; 1889 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCAATCTCGGTGGACACTCTCTCTTGGCCACGAAGCTCATTTCTCG
                                       ; DB 23;
3. 9.8e-06;
3. 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis; Iturin A; cation channel;
                                                                                                                 0; Mismatches
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Matches
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                               \overset{\times}{\times} \overset{\times}
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                                                                   Ø
of the cell through the cation channel of the cell and a promoter for transferring the cation to the exterior of the cell containing Iturin as the active component. The gene can be used for the preparation of Iturin A in a large quantity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             719 TCGCAGGGCAAAGGTTGTACCGAAGCAGCAGACAGCGCGCGGTTACCGACATTTCCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18489 CGGCTCCGGTCAAAAGCGTGACAGCGGCATAGAGTACGTCCCGCCGCAAACTTCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        779 CAGTGAGGTCGAAGTCATTCTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28549 AAATCCAGCTGACAGCAATTTGGGAGGA-----TGTCCTTGGACTAGAGCAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCGAAGICCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28370 CAGTGAACTTCGCGAAAGAATGGCCCGGCATTTACCCGGGATATATGATCCCCGCTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  839 CATTACCGATCACTTCTTCAATCTCGGTGGACACTCTCTTTGGCCACGAAGCTCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGTATCGACCAACGACTCAAGGTCCGTATCACTGTCAAGGATGTCTTTGACCATCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide synthase; soil; lichen; antibiotic biosynthesis; humus;
                                                                                                                                                                                                             Sequence 41599 BP; 12054 A; 9173 C; 10241 G; 10131 T; 0 other;
                                                                                                                                                                                                                                                                                                                    Length 41599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapeutic; immunosuppressor; antitumour agent; pathogen;
                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.00017;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                          0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soil derived peptide synthase clone ps7 DNA.
                                                                                                                                                                                                                                                                                                       Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yap WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| | || ||| ||| |||| 28721 CATTGAACAGCTCGCA 28736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waters B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TERR-) TERRAGEN DIVERSITY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTGCGGATCTAGCA 974
                                                                                                                                                                                                                                                                                                       5.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0861774.
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                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 49.79
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seow KT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-070158/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a DNA sequence which partially encodes the dinctional portion of polypeptide component required for synthesizing the polyketide antibiotic Tel-Aviv, postmodification of antibiotic Tel-aviv, or regulation of blosynthesis of antibiotic Tel-aviv. The antibiotic Tel-aviv is a macrocyclic polyketide synthesised through the incorporation of acetate, methionine, and glycine. It inhibits cell wall synthesis by interfering with the polymerisation of the lipid-disaccharide pentapeptide. Antibiotic Tel-aviv genes are useful in combinatorial genetics, and for encoding protein components for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel DNA sequence involved in polyketide antibiotic Tel-Aviv production useful for inhibiting cell wall synthesis and in wide range of clinical applications such as treating gingivitis
                                                                                                                         method allows access to the reservoir of genetic diversity in soil pathogenic micro-organisms, in order to find new antibiotics. It also allows access to novel biosynthetic genes/enzymes that can be used to produce antibiotics or produce specific compounds, enzymatically,
                                                                                                                                                                                                                                                                                                                                        596 CGCCATCGAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAA
                                 This sequence encodes a peptide synthase clone, isolated from soil. This protein is used in a method for the recovery of antibiotic biosynthetic DNA from humic materials or lichen. The PCR products of invention have the potential to be used as therapeutic molecules including antibiotics, immunosuppressors and antitumour agents. The
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                       Length 1200;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                  Sequence 1200 BP; 197 A; 392 C; 384 G; 226 T; 1 other;
                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a peptide synthetase unit-PKS module.
                                                                                                                                                                                                                                                                     Score 49.6; DB 20;
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell wall synt|
gingivitis; ss
                                                                                                                                                                                                                                                            5.0%; Score ... 3.3e-v
63.3%; Pred. No. 3.3e-v
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     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polyketide; antibiotic Tel-Aviv;
lipid-disaccharide-pentapeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 6-8;,66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000EP-0300747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                    Local Similarity. 63.3
 Claim 17; Page 82-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ron E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-500254/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myxococcus xanthus
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                                                                                                                                                                                              in vitro.
                                                                                                                                                                                                                                                                     Query Match
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830 GAAGGITGACATTACCGATCACTICTTCAATCTCGGTGGACACTCTCTTGGCCACGAA 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence coding for products involved in the biosynthesis of polyketide or heteropolyketide compounds, especially epothilone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 37856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37856 BP; 5655 A; 13666 C; 12913 G; 5622 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product- "ORF13-transcription regulator"
complement (35730..36242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "ORF14-transcription regulator"
/hote= "GTG start codon"
                                                                                                                                                                                                                                                                                         "ORF10-transcription regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "ORF12-regulation element"
complement (35255..35616)
                                                                                                                                                                                                                                                                                                                                                element"
                                                    /product= "ORF6-polyketide synthase"
                                                                                                                                                                                                                   "ORF9-regulation element"
                                                                                                         "ORF7-peptide synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4..8%; Score 48.2; DB 21 ilarity 58.9%; Pred. No. 0.00063; Conservative 0; Mismatches 58
                                                                                                                                                              /product= "ORF8-transpeptidase"
complement (30040..31720)
                                                                                                                                                                                                                                                                                                                                            /product= "ORF11-regulation
/hote= "GTG start codon"
33661..34077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
'note= "ACC start codon"
                                                                                                                                                                                                                               /note= "CGC stop codon
31982..32932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 20-33; 36pp; German.
                                                                                                                          28251..29400
                                                                                                                                                                                                                                                                                                          33128..33613
                    5374..19984
                                                                       20003..27889
                                                                                                                                                                                                                     /product=
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Best Local S
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                                                                                                                                                                                                                                                                                                            726
                                                                                                                                                                                                                                                                                                                                                                                CAAAGGTTGTACCGAAGCAGCAGACAGCACCGCTTACCGACATTTCCCATCAGTGAGG 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                      846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              847 ATCACTICITICAATCTCGGTGGACACTCTCTTGGCCACGAAGCTCATTTCTCGTATCG 906
 synthesis, modification and regulation of antibiotic antibiotic Tel-aviv.
                 Antibiotic Tel-aviv is useful in a wide range of clinical applications such as treating gingivitis. Antibiotic Tel-aviv is also useful for generating new biological agents from its secondary metabolites. The present sequence encodes a protein involved in synthesis of antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polyketide biosynthesis; heteropolyketide biosynthesis; mutasynthesis; epothilone; cytotoxic; immunosuppressant; antibiotic; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                     607 TCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGGATCGAACATCGTTGTTC
                                                                                                                                                                                                                                                                                                                                            1681 TGGATGCGATTCCGCTGTCGGCCAATGGCAAGGTGGACCGGGGCCAGCTGATGGCCAGGC
                                                                                                                                                                                                                                                                                                            787 TCGAAGTCATTCTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "ORF3-aminotransferase"
/note= "AGT start codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. cellulosum DNA encoding polyketide and hereropolyketide enzymes
                                                                                                                                                                                                  6
                                                                                                                                                                Length 7178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "ORF4- tyrosine/DOPA-Decarboxylase"
                                                                                                                          Sequence 7178 BP; 1119 A; 2280 C; 2548 G; 1231 T; 0 other;
                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2912 ACCGGCGTTCGACACGCGCTCGCCGTCACCGACCTGTT 2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCAACGACTCAAGGTCCGTATCACTGTCAAGGATGTCTT 946
                                                                                                                                                            Query Match 4.9%; Score 49.2; DB 21;
Best Local Similarity 50.9%; Pred. No. 0.00012;
Matches 173; Conservative 0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "ORF1-tRNA synthetase"
/note= "gtg start codon"
complement (6374..7111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "ORF2-monooxygenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "GTG start codon"
12212..13658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3398..6100)
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Sanchez C,
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Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.
                                                                                                                                                                       BLM gene cluster; bleomycin gene cluster; polyketide metabolite; bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine; thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                                                        'transl_except= (pos: 1..3, aa: Met)
note= "ORF31; encodes AAB07580"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_except= (pos: 1..3, aa: Met)
/note= "ORF39; encodes AAB07588"
                                                                                                                                                                                                                                                                                                                                                                                                                               transl_except= (pos: 1..3, aa: Met)
note= "ORF37; encodes AAB07586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "ORF40; encodes. AAB07589"
/note= "no termination codon given"
                                                                                                                                                                                                                                                                                           noté= "ORF32; encodes AAB07581"
                                                                                                                                                                                                                                                                                                                                                encodes AAB07583"
                                                                                                                                                                                                                                                                                                                                                                           "ORF35; encodes AAB07584"
                                                                                                                                                                                                                                                                                                                      "ORF33; encodes AAB07582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encodes AAB07587"
                                                                                                                                                                                                                                                                                                                                                                                                      encodes AAB07585'
                                                      19834 rececceaceercecaeger 19854
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                                     950 CCATCCTGTATTTGCGGATCT 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "ORF38;
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                                                                                                  AAA58472 standard; DNA; 18660
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99US-0118848.
2000US-0477962.
                                                                                                                                                                                                                                                                                                                                               'note= "ORF34
                                                                                                                                                                                                                                                                                                                                                                            note= "ORF3
2637..13920
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                                                                                                                                       (first entry)
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                                                                                                                                                                                                            Streptomyces verticillus.
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                                                                                                                                     31-OCT-2000
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05-FEB-1999;
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                                                                                                                    AAA58472;
                                                                                 RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4932 CGCTGTGCACGACGACTTCTTCGAGCTGGCGGGCACTCGTTGCTGGTGGTCGAGGTGAT 4991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   596 CGCCATCGAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              836 TGACATTACCGATCACTTCTTCAATCTCGGTGGACACTCTCTTGGCCACGAAGCTCAT 895
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                                                                                                                                                                                                                                                                               The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 31-40. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiazolidine, thiazoline, bithiazolime and bithiazolime-containing minicabial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4758 GGTGGTCGTCCTGGAGGCGCTGCCACTGACGGAAAGCTGGAACGCTGGACGCCGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTCGCAGGGCAAAGGTTGTACCGAAGCAGCAGACAGCAGCGCCGTTACCGACATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4818 GCCGCCCCCCCCGCGCGCGCAGACCGGAACTGGAT-----GTCCGCTTCGTGGCGCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 CATCAGTGAGGTCGAAGTCATTCTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
P-PSDB; AAB07580, AAB07581, AAB07582, AAB07583, AAB07584, AAB07585,
AAB07586, AAB07587, AAB07588, AAB07589.
                                                                                           New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.8%; Score 48; DB 21; Length 18660; 47.2%; Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18660 BP; 2365 A; 7239 C; 6510 G; 2546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.0005;
0; Mismatches 200; Indels
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                                                                                                                                                                                                                         Claim 8; Page 137-153; 162pp; English.
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nes 184; Conservative
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Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag array
                                        Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
Bacillus licheniformis genomic sequence tag (GST) #2169.
                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVOZYMES BIOTECH INC.
                                                                                                                                                                                                                                                                                                  06-OCT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                                           05-OCT-2001; 2001WO-US31437
                                                                                                                            Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                     Berka R, Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                          NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-416684/44.
                                                                                                                                                                     WO200229113-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in conter Bacillus cells. Comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells. The method is useful for monitoring of spot in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, and in which Bacillus cells adapt to changes in culture conditions, conviconmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is the method of the invention.

The method of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                        Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3662 CGAAATGAGAGGGTCTTTCTGAGCGGCTTCCGTCGTACATGATCCCGTCATATTTCGT
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63.2%; Pred. No. 0.00068;
Live 0; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 2166; 200pp; English.
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                                                                                                                                                                                                                                                       (NOVO ) NOVOZYMES BIOTECH INC. (NOVO ) NOVOZYMES AS.
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27-MAR-2001; 2001US-279526P.
                                                                                                                                              05-OCT-2001; 2001WO-US31437.
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Best Local Similarity bo...
Best Local Similarity
T2; Conservative
                    Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                         Clausen IG;
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in conter Bacillus cells, comprising hybridising labelled nuclaic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genewrespienby an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells relative to expression of the same genes or more second Bacillus cells. The method is useful for monitoring genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring cenes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in which Bacillus cells adapt to changes the culture conditions, in which Bacillus cells adapt to changes the culture conditions, conviconmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence tag (GST) used in the method of the invention.

Specification, but was obtained in electronic format directly from WIPO
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Pred. No. 0.00078;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
Claim 4; SEQ ID NO 2169; 200pp; English.
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Best Local Similarity 63.2
Matches 72; Conservative
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4390

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810 GCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACTTCTTCAATCTCGGTGGA 4337 GIGCICGGCATGGATGGCA----TCGGCGTCCATGATCACTTCTTCGACTCTGGAGGA

CACTCTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTCAAGGT

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Collection of nucleic acids from environmental samples, useful for identifying e.g. genes encoding polyketide synthases and derived antibiotics
                                                          Metabolic pathway operon; polyketide; polyketide antibiotic; type I polyketide synthase; ss.
                                                                                                                       /*tag= a
/product= "type I polyketide synthase"
                                         Nucleotide sequence of a type I polyketide synthase.
                                                                                                                                                                                                                                          Guerineau M,
                                                                                                                                                                                                                                        Jeannin P, Pernodet J, Guerineau M,
Cappellano C, Francou F, Raynal A,
Frostegard A;
                                                                                                                                                                                                                                                                                                                                  Claim 35; Page 300-302; 356pp; French.
                                                                                                   Location/Qualifiers
2..4615
                                                                                                                                                                                               29-NOV-1999; 99FR-0015032. 07-JUN-2000; 2000US-0209800.
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                         (first entry)
                                                                                                                                                                                                                         (AVET ) AVENTIS PHARMA SA.
                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                         WPI; 2001-374849/39.
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                                                                                                                                              WO200140497-A2
                         06-AUG-2001
                                                                                   Unidentified
                                                                                                                                                              07-JUN-2001
        AAF90034;
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Tuphile K;

Simonet P, Courtois S; Ball M, Sezonov G, Tup

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The specification describes a method for the preparation of a collection of nucleic acids from organisms in a soil sample. The method comprises milling a dried sample to produce microparticles; suspending these in liquid buffer: extraction of nucleic acids from the microparticle; passing nucleic acid-enriched fractions through a molecular sleve; passing nucleic acid-enriched fractions through a maion exchange chromatography material; and recovering fractions containing purified nucleic acids. The nucleic acids are sources for sequences that encode either operons involved in a metabolic pathway (specifically polyketide synthesis) or polypeptides, particularly for production of therapeutic or agricultural compounds, especially polyketide antibiotics. AAF90034.39 represent open reading frames (ORFS) of the coding strand of cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     630 CTTCCATCGTACATGATCCCATCGAACATCGTTGTTCTGGACAAGATGCCTCTCAACGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4615 BP; 827 A; 1477 C; 1429 G; 882 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%; Score 45.4; DB 22; 49.8%; Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                              a26g1, and encode type I polyketide synthases.
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Matches 146; Conserv
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CTGCCCGACTACATGATCCCGACCGCGTGGTCGTGCTCCACGAAATGCCGCTGACGCCC 4216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes a method for the preparation of a collection of nucleic acids from organisms in a soil sample. The method comprises milling a dried sample to produce microparticles; suspending these in liquid buffer; extraction of nucleic acids from the microparticle; passing nucleic acid-containing solution through a molecular sieve; passing nucleic acid-enriched fractions through a molecular sieve, chromatography material; and recovering fractions containing purified nucleic acids. The nucleic acids are sources for sequences that encode either operons involved in a metabolic pathway (specifically polyketide synthesis) or polypeptides, particularly for production of therapeutic a agricultural compounds, especially polyketide antibiotics. The present sequence represents cosmid a2691 coding strand), which encodes different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pernodet J, Guerineau M, Simonet P, Courtois S;
;, Francou F, Raynal A, Ball M, Sezonov G, Tuphile K;
Collection of nucleic acids from environmental samples, useful for identifying e.g. genes encoding polyketide synthases and dérived antibiotics \cdot
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                                                                                                                                                                                                                                                                                                                      Metabolic pathway operon; polyketide; polyketide antibiotic;
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                                                                                                                                                                                                                                                                         Nucleotide sequence of cosmid a26g1 (coding strand).
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Pred. No. 0.0048;
0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 14; Page 289-300; 356pp; French.
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Best Local Similarity
Matches 146; Conserva
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Cappellano C, E
Frostegard A;
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                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                        RESULT 14
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                                                                                                                                                                                                       4337 GTGCTCGGCATGGATGGCA-----TCGGCGTCCATGATCACTTCTTCGACTCTGGAGGA
                              750 ACAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTCATTCTTTGCGAAGAA
                                                                                                                                                              GCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACTTCTTCAATCTCGGTGGA
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Ball M, Sezonov G, Tuphile K:
                                                                                                                                                                                                                                                                                                                               Collection of nucleic acids from environmental samples, useful for identifying e.g. genes encoding polyketide synthases and derived antibiotics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metabolic pathway operon; polyketide; polyketide antibiotic; ss.
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                                                                                                                                                                                                                                                                                         870 CACTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTCAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of cosmid a26g1 (non-coding strand)
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C, Francou F, Raynal A,
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ID AAF90032 standard; DNA; 42717 BP.
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Frostegard A;
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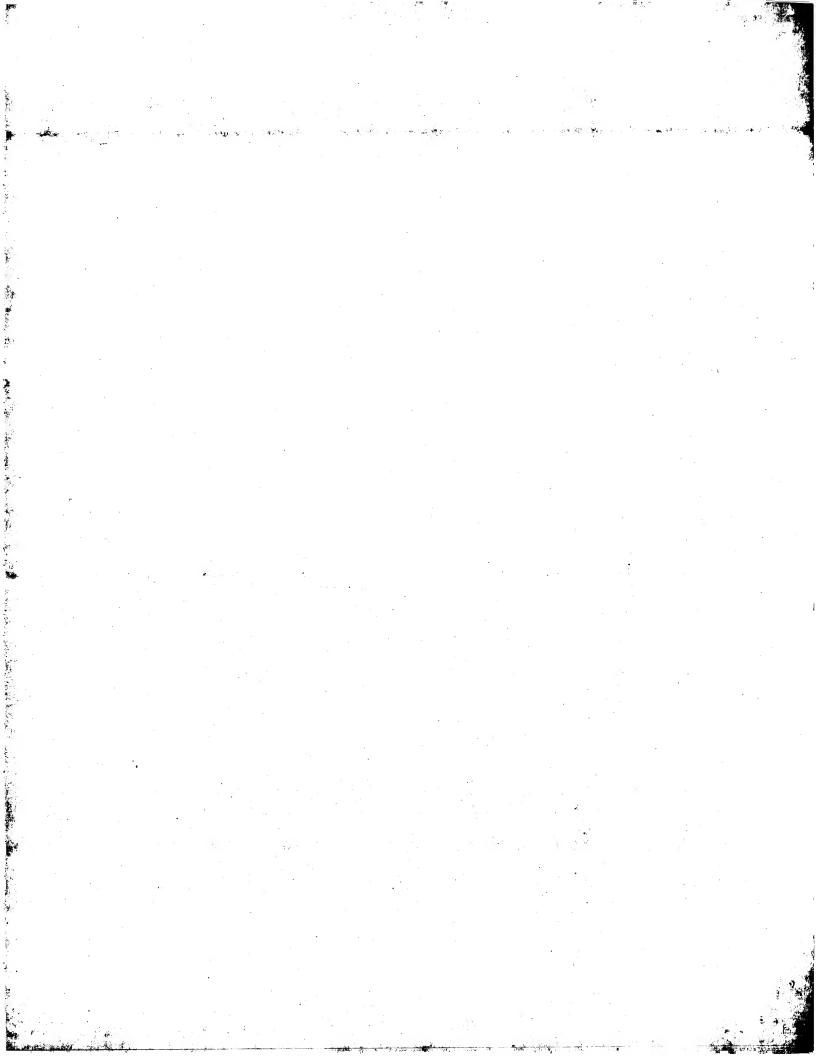
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29843 GAAGCATICACGCCTCCGGAAACTCCGGTGGAACAGGTACTCGCCCACATTTGGGGCGAG 29784
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Score 240.2; DB 1; Length 46899;
Pred. No. 1.1e-69;
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APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
US-08-961-527-167
US-08-147-777-3
US-08-147-777-3
US-08-128-872-87-3
US-08-961-774E-83
US-08-963-602-6
US-08-963-774E-81
US-09-134-001C-2065
US-09-144-476-64
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US-09-142-6178-1
US-09-145-7028-1
US-09-145-7028-7
US-09-145-7028-7
US-09-453-7028-7
US-09-453-7028-7
US-09-453-7028-7
US-09-453-7028-7
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APPLICANT: Lettner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Meber, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5527706artis Corporation
STREET: 59 Route 10
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08471119A Patent No. 5827706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFRENCE/DOCKET NUMBER: 100-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 46899 base pairs
TYPE: nucleic acid
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ATCC 34921
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CITY: East Hanover
STATE: New Jersey
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Best Local Similarity
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US-08-471-119A-1
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Sequence 24, Appl
Sequence 627, App
                                                                                                         (without alignments)
5385.674 Million cell updates/sec
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                                                                                      June 4, 2003, 19:04:47; Search time 57 Seconds
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-861-774E-17
US-08-861-774E-91
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US-09-567-899-1
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US-09-568-486-1
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Listing first 45 summaries
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                       1 AACCIGCTITCTTCACCTCGTTGAAAGACAGGTTTCCAGGTCTGGTGGAACATGTTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 189.2; DB 1;
Pred. No. 2.2e-53;
0; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100-8029/CONT/CONT
                                                                                                                                      Cyclosporin Synthetase
                                                                                                                                                                                SSEE: No. 5827706artis Corporation
F: 59 Route 10
East Hanover
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                             APPLICANT: Leitner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schoergendorfer, Kurt
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Syr
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Necosmospora vasinfecta
                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                Sequence 4, Application US/08471119A
Patent No. 5827706
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: KASSENDOFÉ, MELVYN
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8874
TELEPHONE: 201 503 8807
                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
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59.5%;
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nucleic acid
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                 GENERAL INFORMATION:
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ORIGINAL SOURCE
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Best Local Simi
Matches 396;
US-08-471-119A-4
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STATE:
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APPLICANT: Light, James
APPLICANT: Molnar, Istvan
APPLICANT: Molnar, Istvan
APPLICANT: Cyr, Ross
APPLICANT: Goerlach, Joern
TILE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFRENCE: 4-30582A
FILE REFRENCE: 4-30582A
FILE REFRENCE: 4-30582A
FILE REFRENCE: 1909-06-10
FRIOR FILING DATE: 2000-05-10
FRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 68750;
                  APPLICANT: ZIKHLE, ROSS
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Josen
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
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Pred. No. 0.059;
0; Mismatches 51; Indels
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Patent No. 6346404
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA; ORGANISM: Sorangium cellulosum
US-09-335-409-1
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Best Local Similarity 57.9%;
Matches 70; Conservative
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Conservative
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
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Best Local Similarity
Matches 70; Conserva
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   TACTTCCATCGTACATGATCCCATCGAACATCGTTGTTCTGGACAAGATGCCTCTCAACG
                                                                                                               CCAATGGTAAAGTTGACCGGAAGGAACTCTCTCGCAGGGCAAAGGTTGTACCGA-AGCAG
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63.3%; Pred. No. 1.8e-06;
Live 0; Mismatches 44; Indels 0
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Best Local Similarity 63.39
Matches 76; Conservative
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APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
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US-09-568-486-1
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Pred. No. 0.059;
0; Mismatches 51; Indels 0;
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Pred. No. 0.059;
0; Mismatches 51; Indels 0;
                                                                                    APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE, REFERENCE: 430582A
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
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                               Sequence 1, Application US/09567969
Patent No. 6355457
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Best Local Similarity 57.9%;
Matches 70; Conservative
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Best Local Similarity 57.9%;
Matches 70; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
                                                                        GENERAL INFORMATION:
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; ORGANISM: SO
US-09-568-480-1
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US-09-568-480-1
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595 TCGCCATCGAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCATCGA 654
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Pred. No. 0.059;
0; Mismatches 51; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Molnar. Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 4-30582A
CURRENY APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 4-30382A
CURRENT APPLICATION NUMBER: US/09/568,472
                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09568486
Patent No. 6355459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09568472 Patent No. 6358719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA CRGANISM: Sorangium cellulosum US-09-568-486-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.9%;
Best Local Similarity 57.9%;
Matches 70; Conservative
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PRIOR FILLING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molnar, Istvan
Zirkle, Ross
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
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LENGTH: 68750
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SEQ ID NO 2
LENGTH: 71989
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                                                                                                                                                                                          595 TCGCCATCGAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGA
                                                                                                                                                                                                                                                                3.9%; Score 39.4; DB 4; Length 68750; llarity 57.9%; Pred. No. 0.059; Conservative 0; Mismatches 51; Indels 0;
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APPLICANT: ZIKEL, BOSON
APPLICANT: GOSTIACH, JOSEN
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,899
FILOR APPLICATION DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
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Patent No. 6303342
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Patent No. 6383787
GENERAL INFORMATION:
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                                              ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-472-1
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US-09-567-899-1
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SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
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                                                                                                                                        Best Local Similarity
Matches 70; Conserv
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              SEQ ID NO 1
LENGTH: 68750
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Fatent No. 6297007
General Information
APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Mio, Yap
APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEO ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
                                                                 TITLE OF INVENTION: Recombinant Methods and Materials for Producing TITLE OF INVENTION: Recombinant Methods and Materials for Producing TITLE OF INVENTION: Epothilone and Epothilone Derivatives FILE REFERENCE: 30062-20031.00

CURRENT APPLICATION NUMBER: US 60/130,560

PRIOR APPLICATION NUMBER: US 60/130,560

PRIOR APPLICATION NUMBER: US 60/122,620

PRIOR PILING DATE: 1999-03-03

PRIOR APPLICATION NUMBER: US 60/119,386

PRIOR APPLICATION NUMBER: US 60/119,386

PRIOR APPLICATION NUMBER: US 60/119,401

PRIOR FILING DATE: 1999-02-10
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US-08-861-774E-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39.4; DB 4; Length 71989;
Pred. No. 0.061;
0; Mismatches 51; Indels 0;
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Pred. No. 0.0055;
0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic construct US-09-443-501A-2
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 57.3%;
Matches 71; Conservative
                                                Ziermann, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.99
Best Local Similarity 57.99
Matches 70; Conservative
Khosla, Chaitan
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 22
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                      TELEX: 899149
TELEX: 890109
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                             linear
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                                                                        FILING DATE:
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602 CGAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGT 661
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                       APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Clone ps25 US-08-861-774E-91
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APPLICANT: SCHETELINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILLING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                      Sequence 91, Application US/08861774E Patent No. 6297007
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5670367
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
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OPERATING SYSTEM:
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                                                                                                                    716 CTCT 719
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LENGTH: 1178
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361 CCGAGGGCGAGTCATCACTATCCGTTCCCGACATCTTTCGCATTGCTGGGGAAGCCGGGT 420
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBBERCHICASIS
FILE REFERENCE: 24366-20007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                 30472/114 IMMU
APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY, AGGNT INPORMATION:
NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REFERENCE/DGCKET NUMBER: 30472/114 IMM TELECOMMUNICATION INPORMATION:
TELEFAN: (703)836-9300
TELEFAX: (703)883-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 ITGTTCTGGACAAGATGCCTCT 682
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; Sequence 2, Application US/09103840A
; Patent No. 6294328
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SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 4403765

TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2
                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                               Query Match 3.8%; Score 37.6; DB 4; Length 4403765; Best Local Similarity 61.0%; Pred. No. 3.1; Matches 61; Conservative 0; Mismatches 39; Indels 0; C
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Job time: 74 secs
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    (without alignments)
    8240.805 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                          870385 seqs, 699768693 residues
                                                                                                                                                                              US-09-482-788-1_COPY_7000_8000
                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                     Run on:
                                                                                                                                                                                                 Title:
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## 1: /cgn2\_6/ptodata/2/pubpna/USO7\_PUBCOMB.seq:\* 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\* 3: /cgn2\_6/ptodata/2/pubpna/NSO6\_PUB\_Seq:\* 4: /cgn2\_6/ptodata/2/pubpna/USO6\_PUB\_OMB.seq:\* 5: /cgn2\_6/ptodata/2/pubpna/USO7\_NEW\_PUB.seq:\* 6: /cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\* 7: /cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\* 8: /cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\* 9: /cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\* 10: /cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\* 11: /cgn2\_6/ptodata/2/pubpna/USO8\_PUBCOMB.seq:\*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published\_Applications\_NA:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	° Query Match Length DB	DB	di	Description
-	53	5.3	13029	10	US-09-815-242-4052	Sequence 4052, Ap
7	49.6	5.0	1200	10	US-09-924-256A-85	Sequence 85, Appl
e	46.8	4.7	6465	10	US-09-974-300-2166	
4	46.8	4.7	8268	10	US-09-974-300-2169	Sequence 2169, Ap
5	42.8	4.3	88421	6	US-09-976-059-1	
9	40.4	4.0	7347	10	US-09-815-242-7773	Sequence 7773, Ap
7	39.8	4.0	3798	10	US-09-974-300-2175	Sequence 2175, Ap
œ	39.8	4.0	3798	10	US-09-974-300-2193	Sequence 2193, Ap
σ	39.4	3.9	68750	6	.US-10-014-717-1	Sequence 1, Appli
c 10	39.2	3.9	1172	10	US-09-924-256A-17	
c 11	38.8	3.9	1178	10	US-09-924-256A-91	
c 12	38	3.8	1160	σ	US-10-123-155-234	
13	37.2	3.7	499	σ	US-10-184-644-592	Sequence 592, App
14	37.2	3.7	499	6	US-10-184-634-592	Sequence 592, App
15	36.4	3.6	513	σ	US-10-123-155-536	Sequence 536, App
c 16	36.2	3.6	547	6	US-10-066-543-1765	Sequence 1765, Ap
c 17	36.2	3.6	4541	6	US-10-123-036-3	
c 18	36.2	3.6	4541	10	US-09-880-107-3785	
19	35.6	3.6	290	10	US-09-294-093B-2985	Sequence 2985, Ap

Seguence 43, Appl	Sequence 1, Appli	Sequence 2167, Ap	Sequence 2566, Ap	Sequence 3817, Ap	Sequence 3926, Ap		96,	3,	Sequence 346, App	Sequence 346, App	÷	Sequence 135, App	Sequence 191, App	Sequence 6617, Ap	Sequence 1, Appli	Sequence 2171, Ap	Sequence 21047, A	Sequence 1125, Ap	Sequence 1126, Ap	Sequence 9039, Ap	Sequence 223, App	Sequence 93, Appl	Sequence 112, App	Sequence 433, App	Sequence 9546, Ap
US-10-166-087-43	US-10-166-087-1	) US-09-974-300-2167	US-10-060-036-2566	US-08-781-986A-3817	US-08-781-986A-3926	US-08-781-986A-206		O US-09-924-256A-23	US-10-184-644-346	US-10-184-634-346	US-09-833-381-134	O US-09-833-381-135	OS-09-923-876-191	_	_	US-09-974-300-2171	US-09-918-995-21047	0 US-09-833-381-1125	J US-09-833-381-1126	US-10-198-846-9039	0 US-09-962-832-223	0 US-09-924-256A-93	US-10-123-155-112	US-09-764-868-433	US-09-815-242-9546
6	σ	10	δ	7	7	7	6	10	9	6	7	7	10	6	7	10	6	H	ï	6	10	7	6	6	7
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3.6	3.6	3.5	3.5	3.5	3.5	3,5	3.5	3.5	3.4	3.4	3.4	3.4	3,3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3,3	3,3	3.3
35.6	35.6	35.4	35.2	35.2	35.2	35.2	34.6	34.6	34	34	33.6	33.6	33.4	33.4	33.4	33.4	33.2	33.2	33.2	33.2	33.2	32.8	32.6	32.6	32.6
20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45
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## ALIGNMENTS

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US-09-815-242-4052
Sequence 4052, Application US/09815242
Sequence 4052, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Racit L.
APPLICANT: Oblised, Racit L.
APPLICANT: Travick, Join D.
APPLICANT: Travick, Join D.
APPLICANT: Travick, Join D.
APPLICANT: Van H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION NUMBER: 60/20/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/20/818
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/25/91
PRIOR RILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25/91
PRIOR RILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SSCFWARE: FRASTSEQ for Windows Version 4.0
SSCFWARE: FRASTSEQ for Windows aeruginosa
US-09-815-242-4052
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Ouery Match 5.3%; Score 53; DB 10; Length 13029; Best Local Similarity 51.9%; Pred. No. 7.9e-07;

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US-09-974-300-2166
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                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                 LENGTH:
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                                                        12707 GCCAGATGCAGAACCAGGCC-----TACCAGGCCCCGCGCAACGAACTGGAGGAAA 12757
                                                                                                                                                                                                                                                                                    12758 CCCTGGCGCGCATCTGGGCCCGAGGTGCTGAGGTCGAGCGGGTCGGGGTGTTCGACAACT 12817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 CGCCATCGAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 AGAGGCTTCGGTCCTTACTTCCATCGTACATGCCATCGAACATCGTTGTTCTGGACA
                                                                                                                                                                           733 TTGTACCGAAGCAGCAGACAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAG
                                                                                                       TCATTCTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Waters, Barbara
APPLICANT: Waters, Barbara
APPLICANT: Waters, Barbara
APPLICANT: Waters, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/09/924,256A
FRIGN APPLICATION NUMBER: US/09/924,256A
FRIGN APPLICATION NUMBER: 08/861,774
PRIOR FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Clone ps30 US-09-924-256A-85
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     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Berra, Randy M.
APPLICANT: Berra, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression.
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
   Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
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illarity 63.3%; Pred. No. 3e
Conservative 0; Mismatche
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Patent No. US20020146721A1
GENERAL INFORMATION:
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Conservative
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Best Local Similarity
Matches 76; Conserv
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LENGTH: 1200
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Matches
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3662 CGAAATGAGAGAGAGTCTTTCTGAGCGGCTTCCGTCGTACATGATCCCGTCATATTTCGT 3721
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                                                                                                                                                                                                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                                                                                                                                          602 CGAAGTCCGCGAGGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGT
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                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3722 AACGGTGGATAAAATGCCGCTTGCGGCGAACGGAAAAGTGGACCGCACGCGCGT 3775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
*FILE REFERENCE: 3019-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                      DB 10;
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Pred. No. 8.6e-05;
                                                                                                                                                                                                                                                                                 Score 46.8; DB 10
Pred. No. 7.4e-05;
0; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GREEAL INCORNATION:
APPLICANT: Clausen, Ib Groth
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-03.
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PLING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR PELING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2169, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09976059; Patent No. US20020164747A1; GENERAL INFORMATION:
                                                                                                                                                                                        TYPE: DNA ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bacillus licheniformis
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                                                                                                                                                                                                                                                                                                                               72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 63.2
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                         Best Local Similarity
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us-09-482-788-1\_copy\_7000\_8000.rnpb

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NAME/KEY: misc_feature
LOCATION: (15203)..(13614)
OTHER INFORMATION: ORF 10; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (15591)..(15863)
OTHER INFORMATION: ORF 11; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (65826)..(66530)
OTHER INFORMATION: ORF 15; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (15880). (19035)
OTHER INFORMATION: ORF 12; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (19032)..(39713)
OTHER INFORMATION: ORF 13; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (39713)..(65800)
OTHER INFORMATION: ORF 14; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (73439). (71964)
OTHER INFORMATION: ORF 20; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (66546)...(67370)
OTHER INFORMATION: ORF 16; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: ORF 18; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (9691)...(10761)
OTHER INFORMATION: ORF 7: positive strandedness
NAME/EXINSC_feature
LOCATION: (12751)...(10829)
OTHER INFORMATION: ORF 8; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (13617)..(12802)
OTHER INFORMATION: ORF 9; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                   ION: (4038)..(5048)
INFORMATION: ORF 3; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (4038)..(5048)
OTHER INFORMATION: ORF 3; positive strandedness
                                                                                                                                                                                                                                                                                        positive strandedness
                                                                                                                                                                                                                                                                                                                                                                  positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (6665)..(5814)
OTHER INFORMATION: ORF 4; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (7703)..(6693)
OTHER INFORMATION: ORF 5; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: ORF 6; negative strandedness
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PAtentIn version 3.0
                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (2077)..(3078)
OTHER INFORMATION: ORF 1; pc
NAME/KEY: misc_feature
LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2; pc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19;
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LOCATION: (70099)..(70662)
                                                                                                                                                   TYPE: DNA
ORGANISM: Actinoplanes sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (6665)..(5814
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                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (4038)..(504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (9464)..(813
                                                                                                  SEQ ID NO 1
LENGTH: 88421
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606 GTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATGTTGTT
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; LCCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27; negative strandedness
LOCATION: (82346)..(82062)
OTHER INFORMATION: ORF 28; negative strandedness
NAME/KEY: misc_feature
LOCATION: (82587)..(8446)
OTHER INFORMATION: ORF 29; positive strandedness
OTHER INFORMATION: ORF 29; positive strandedness
                                                                                                                     LOCATION: (75535)..(76464)
OTHER INFORMATION: ORF 23; positive strandedness NAME/KEY: misc_feature
LOCATION: (78110)..(76449)
OTHER INFORMATION: ORF 24; negative strandedness
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (81624)..(79861)
OTHER INFORMATION: ORF 26; negative strandedness
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LOCATION: (85556)..(86845)
OTHER INFORMATION: ORF 31; positive strandedness
                  NAME/KEY: misc_feature
LOCATION: (75424)..(74213)
OTHER INFORMATION: ORF 22; negative strandedness
                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25; negative strandedness
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LOCATION: (84481). (85548)
OTHER INFORMATION: ORF 30; positive strandedness
INFORMATION: ORF 21; negative strandedness
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LOCATION: (87372)..(86803)
OTHER INFORMATION: ORF 32; positive strandedness
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7773, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamcto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck, Robert
                                                                                             NAME/KEY: misc_feature IOCATION: (75535)..(76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
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APPLICANT:
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APPLICANT:
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2858 AGCGCCGTGC------ACCCCGCAATGCTACGGAAGAAAGCTTGCAGTGATT 2904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2858 AGCGCCGTGC------ACCCCGCAATGCTACGGAAGAAAGCTTGCAGTGATT 2904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           750 ACAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTCATTCTTTGCGAAGAA 809
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                                                                          750 ACAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTCATTCTTTGCGAAGAA
                                                                                                                                                                                                      810 GCCACTGAGGTGTTTGGCA---TGAAGGTTGACATTACCGATCACTTCTTCAATCTCGGT
                                                                                                                                                                                                                                                                    GGACACTCTCTTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTCAAGGTCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REPERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2010-03-27
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Pred. No. 0.015;
0; Mismatches 162;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 2193, Application US/09974300
Patent No. US/20020146721a1
GENERAL INFORMATION:
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ilarity 50.7%;
Conservative
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Best Local Similarity
Matches 185; Conserva
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Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT FILING ANTE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
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Pred. No. 0.013;
0; Mismatches 71;
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Pred. No. 0.015;
0; Mismatches 162;
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              PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 14110
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2175
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PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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; ORGANISM: Bacillus licheniformis
US-09-974-300-2175
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Best Local Similarity 53.9%;
Matches 83; Conservative
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Best Local Similarity 50.7%;
Matches 185; Conservative
APPLICATION NUMBER:
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US-09-815-242-7773
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LENGTH: 7347
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Query Match 3.9%;
Best Local Similarity 57.3%;
Matches 71; Conservative
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Beresini,Maureen
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity
                                                                                                                                                                                                                                                                                 153 GCCT 150
                                                                                                                                                                                                                                                  716 CTCT 719
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APPLICANT:
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APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
CURRENT FILING DATE: US/09/924,256A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 08/861,774
PRIOR FILING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 68750;
                                                                                                                                                                                                                                                                             APPLICANT: Cyr, Devon
APPLICANT: GGELIACH, JOERN
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
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Pred. No. 0.11;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/014,717 CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09924256A
Patent No. US20020127659A1
                                                                                                                                                               Sequence 1, Application US/10014717 Publication No. US20020192778A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-10-014-717-1
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ORGANISM: Artificial Sequence
FEATURE:
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1 Similarity 57.9%;
70; Conservative
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SEQ ID NO 1
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SEQ ID NO 17
                                                                                                                                                                                                                                 Ligon, James
Molnar, Istvan
Zirkle, Ross
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APPLICANT: Miao, Vivian
                                                                                                                                                                                                              APPLICANT: Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NOS:
                                                                    11111
3085 CAAGG 3089
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Matches 70; Conserv
                                                CAAGG 991
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                                                                                                                                                                                                                                                        602 GGAAGTCCGCGAGAGGCTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGT
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APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Ton, Yap
APPLICANT: Ton, Yap
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Clone ps25 US-09-924-256A-91
; OTHER INFORMATION: Description of Artificial Sequence: Clone ps32 US-09-924-256A-17
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Pred. No. 0.016;
0; Mismatches 47;
                                                                   Score 39.2; DB 10;
Pred. No. 0.012;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/09/924,256A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 08/861,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 91, Application US/09924256A Patent No. US20020127659A1
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Wood, William I.
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                           Zhang, Zemin
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                                                                                                                                                                                           Chen, Jian
                                                                                                                                                                                                                                                                             Pan,James
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nes 36; Conserv
                                                                                                  US-10-184-644-592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATTGCTGGGGAAGCCGGGTTCCGTGTCGAGGTCAGTTCTGCACGACAGTGGTCTCAGA 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 ACATGATCCCATCGAACATCGTTCTTGGACAAGATGCCTCTCAACGCCAATGGTAAAG 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533 .TA.CTD..BAWYRABM...MTB.C.RSSCHNRBAC.RHM.R.BCD..KS...STYNR.B 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         893 M.HBTSRR.WSBGTSHN.C.CSY...NW.RABB.C..TT..WBAAS..BCDTDBSR.YS
                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 CGCTTGAGAAGATGACTGGATCGACTTTCAAGCGAATCAATTGAACCAGAAGTCACTGG
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Pred. No. 0.031;
13; Mismatches 470; Indels
                                                                                                                                                                                                                    See Palm or File Wrapper
                                                                                                                                                            FILE REFERENCE: P3330RIC30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                        Conservative 213;
                            Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                      Query Match 3.8%;
Best Local Similarity 9.1%;
                                                                                Watanabe, Colin K
                                                                                                                                                                                                                  Prior Application removed - NUMBER OF SEQ ID NOS: 550
                                                                                                Wood, William
                                                                                                                                                                                                                                                                                                        Homo Sapien
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138 CTTGGAGATGAGCTTGTGCTTCCGGTTGAGAAGATGACTGGATCGACTTTCAAGCGAAT 197
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NUMBER OF SEQ ID NOS: 612
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llarity 9.5%; Pred. No. 0.036;
Conservative 113; Mismatches 228;
353 NB.GS..WAC..W.BK.TAB.AT...NTBHA 323
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CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                               Sequence 592, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
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GENERAL INFORMATION: APPLICANT: BARET, KEVIN P.
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                                                                                                                                                                                                                                                                           Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/184,634 CURRENT FILING DATE: 2002-06-28
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o. US20030068794A1
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Wood, William I.
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Beresini, Maureen
                                                   Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                        Pan, James
Smith, Victoria
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                                   Soddard, Audrey
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                                                                                                                                                                   Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-592
Chen, Jian
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                                                                                                                                                                                                                                                                                                                  SEQ ID NO 592
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                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333OHD NUMBER: US/10/123,155
CURRENT APPLICATION NUMBER: 2002-04-15
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Stewart, Timothy A.
                                                             Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                       ; Prior Application removed ; · NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-155-536
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BE492765 WHE0564\_E AL185787 Tetraodon AL385769 MtBC30E07

744 bp DNA linear GSS 09-SEP-1998 mgxb0023A03r CUGI Rice Blast BAC Library Magnaporthe grisea genomic aClone mgxb0023A03r, DNA sequence. BF809723 CM1-CT013 BF009470 CM4-UT000 BM044659 603622365 BM044732 603622365 BM044732 603622473 BG823879 603722953 BQ900191 AGENCOURT BQ919273 AGENCOURT BQ9167759 QH819A10. BG31800 ZM32333 AGENCOURT BQ9167759 QH819A10. BG31800 ZM32333 AGENCOURT BQ917781 AGENCOURT BQ177781 AGENCOURT BL114975 OSTF063C7 C08494 C08494 Yuji BB656627 BB656627 AW740666 ur04e12.y ALO74375 Drosophil ALO74375 Drosophil BE999591 EST431314 BO702499 NXSI 129\_ BO655623 NXRV096\_H AQ362655 NXRV096\_H AQ362655 NXRV096\_H AQ362655 NXRV096\_H AQ3653 NXRV096\_H AQ365751 NXSI\_008\_ BF77071 MXSI\_008\_ AL377071 MXBE99810 C18042 C18042 Huma AL167296 Tetracdon BI192067 14912fs.f AA272108 va42f09.r AL581888 AL581888 Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe. 100 Jordan Hall, Člemson Universiy, Clemson, SC 29634 Tel: 864 656 5737 Fax: 864 656 4293 Contact: Dean RA Clemson University Genomics Institute Clemson University ALIGNMENTS Seg primer: GGAAACAGCTATGACCATG Class: BAC ends High quality sequence stop: 431. Location/Qualifiers CNS028CI AL385769 BF809723 BF094070 AW740666 CNS00139 AL372468 BM044659 BM048043 BM044732 BG823879 BQ900191 BQ936677 BQ277781 BI174975 BE999591 BQ702499 BG319806 Email: rdean@clemson.edu AQ163140.1 GI:3559541 117 117 117 117 117 Magnaporthe grisea. Magnaporthe grisea 1 (bases 1 to 744) Unpublished (1998) 812 1050 653 Genome AQ163140 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION REFERENCE AUTHORS JOURNAL RESULT 1 TITLE COMMENT 000000000 AQ163140 mgxb0023A AQ990481 Rfc01258 AQ990701 Rfc01513 AL43321 T7 end of AL433819 T7 end of AQ989957 Rfc00641 (without alignments) 9488.839 Million cell updates/sec No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. aacctgctttcttcacctcg......tccgtcaagggctgggtttg 1001 Description 4, 2003, 17:53:27; Search time 1708.5 Seconds 32308132 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. 16154066 segs, 8097743376 residues Total number of hits satisfying chosen parameters: US-09-482-788-1\_COPY\_7000\_8000 1001 SUMMARIES Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries AQ163140 AQ990481 AQ990701 CNS077YR CNS078CL AQ989957 nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 П em\_gss\_mus:\* em\_gss\_other: length: 0 length: 2000000000 em\_gss\_rod:\* gb\_est3:\*
gb\_est4:\*
gb\_est5:\*
em\_estfun:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_fun:\* em\_gss\_mam:\* em\_gss\_pro:\* em\_estom:\* gb\_gss:\* DB em\_esthum:\* em\_estro:\* em\_htc:\* gb\_est2:\* gb\_htc:\* em\_estba:\* em\_estin:\* em\_estpl: em\_estmu: gb\_est1:\* Query Match Length em\_estov 606 632 850 1040 708 EST:\* June greater or in Pred. No. sed Title: Perfect score: Scoring table: Score score gand is DB OM nucleic Sequence: Searched: Database Maximum Run on: Minimum Result No. 400

FEATURES

BE052874 GA\_Ea003 BG531334 602559574 AL178252 Tetraodon BB721296 BB721296

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french-Constant,R.H., Materfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Erviron. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                            835 ITGACATTACCGATCACTTCTTCAATCTCGGTGGACACTCTCTTTGGCCACGAAGCTCA 894
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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

116 c 120 g 204 t 3 others
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Department of Biology and Biochemistry
Diniversity of Bath
South Building, Bath BAZ 7AY, UK
Tel: (44) 1225 826621
Email: bassfr@dath.ac.uk
Email: bassfr@dath.ac.uk
This is one of 2.122 random reads from the MI3 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
Coli KIZ genome) please see ffrench-Constant et al. 2000, Nucleic
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             895 ITTCTCGTATCGACCAACGACTCAAGGTCCGTATCACTGTCAAGGATGTCTTTGACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ990701 632 bp DNA linear GSS 14-AUG
Rfc01513 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01513, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="PLG01513"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                               /clone_lib="Photorhabdus luminescens strain W14 M13
                                                                                                                                                                                                                                                                                                    Length 606;
                                                                                                                                               /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size
kb) and then cloned into M13 Janus."
122 c 115 g 174 t 3 others
                                                                                                                                                                                                                                                                                                                                                71; Indels
/organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                             Score 40.4; DB 17;
Pred. No. 1.4;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            955 CTGTATTTGCGGATCTAGCATCTGTCATCCGTCA 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAACCATTGCTCAGATTGCCAGTGTGATTCGCCA 421
                                                /db_xref="taxon:29488"
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                                                                       /clone="PLG01258"
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Class: shotgun,
                       /strain="W14"
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                                                                                                                                                                                                                                                                                               ch 4.0%;
1 Similarity 53.9%;
83; Conservative
                                                                                                                           library"
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                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 83
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LOCUS
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KEYWORDS
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                                                                                                                                                                                 Another "Vector: Data With Site. 1: HindIII; Site. 2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n-7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request.
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ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blatiner,P.R.
A genomic Sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGTCGTATGCAGGCTGAGCTTCGCGACCATCTCAAGTCAAGGTTGCCGACCTACGCCG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              646 TCCCATCGAACATCGTTGTTCTGGACAAGATGCCTCTCAACGCCAATGGTAAAGTTGACC 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Photorhabdus luminescens
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ990481 606 bp DNA linear GSS 14-AUG
Rfc01258 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01258, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 744;
                                                                                       /clone="mgxb0023A03r"
/clone=lhb="Cog1 Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
            /organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.2; DB Pred. No. 0.94; 0; Mismatches
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1..606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.18;
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AQ990481.1 GI:9649075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 56.7
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photorhabdus.
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907

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL MEDLINE

TITLE

DEFINITION

RESULT 2 AQ990481

ACCESSION

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FEATURES

Query Match

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BASE COUNT

ORIGIN

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Query Match

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RESULT 4 CNS077YR/C LOCUS

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ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE

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Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
3 seqreféqenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, ¿Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces angusts, Debaryomyces hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 TTCTTTGACCTGGGTGGACACTCGATCCTCGCCACGCGGATGTTTTGAGTTGAGAAAA 425
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Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
                                                              complement(<3. .>796)
/note="similar to Saccharomyces cerevisiae ORF YBR115c LYS2; L-aminoadipate-semialdehyde dehydrogenase, large
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Souciet, J. L., Aigle, M., Artiguenave, P., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Sautin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
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FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              852 TTCTTCAATCTCGGTGGACACTCTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.8; DB 17; Length 850;
Pred. No. 2.8;
0; Mismatches 57; Indels 0
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                                                                                                                                                                subunit ]
1 putative frameshift(s)"
/evidence-not_experimental
- 227 c 221 g 209 f
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/clone_lib="BB0AA"
                                   /note="end : T7"
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AL433819.1 GI:12217233
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Best Local Similarity 56.5
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   972 GCATCTGTCAT 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 850 bp DNA linear GSS 08-JUL-2001 end of clone BBOAA015F05 of library BBOAA from strain CBS 4732 Pichia angusta, genomic survey sequence.
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                                                                                                                                                                                                                      894
                                                                                                                                                                                                                                                             895 TITCICGIATCGACCAACGACTCAAGGICCGIATCACTGICAAGGAIGICTTIGACCAIC 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 850)
Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
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the other extremity of this insert.
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Saccharomycetales; Saccharomycetaceae; Pichia.
1 (bases 1 to 850)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Souchet, J. L., Algle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Sautin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Mincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                  835 TTGACATTACCGATCACTTCTTCAATCTCGGTGGACACTCTCTTTGGCCACGAAGCTCA
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                                                                          Length 632;
                                                                                                                                                Indels
                                                                                                                                    71;
                                                                      DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40.4; DE Pred. No. 1.4; O: Mismatches
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/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0AA015F05"
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                                                                                                     Best_Local Similarity 53.9
Matches 83; Conservative
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TITLE JOURNAL

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AUTHORS

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REFERENCE

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/clone="PLG00641"
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Similarity 52.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 852 ITCTTCAATCTCGGTGGACACTCTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                   912 CGACTCAAGGTCCGTATCACTGTCAAGGATGTCTTTGACCATCCTGTATTTGCGGATCTA 971
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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coll K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                      this sequence and for the sequence of
                                                                                                                                                                                                     /note="similar to Saccharomyces cerevisiae ORF YBR115c LYS2 ; L-aminoadipate-semialdehyde dehydrogenase, large subunit ]"
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Rfc00641 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00641, DNA sequence.
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5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequent the other extremity of this insert.

Location/Qualifiers
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/db_xref="taxon:29488"
                                                                                                                                                                                                                                                                                                                                                                           57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                   /organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BBDAA019F07"
/clone=lib="BBDAA"
/note="end : T7"
/s. > 1027
/note="similar to Saccharomy
                                                                                                                                                                                                                                                                                                                                            Score 39.8; DE
Pred. No. 3.3;
0; Mismatches
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262 c 287 g 234
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Best Local Similarity 56.5%;
Matches 74; Conservative (
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Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific Mest Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Anderson, O.D., Chao, S., Dubcovsky, J., Echenique, V., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., Stamove, B. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes: Vegetative apex cDNA library from Triticum monococcum
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                                                  /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
150 c 152 g 183 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                     874 CTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTCAAGGTCCGTATCACTG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 CAGTGTTGGCGTTAGTCAAGTCGGCATTTATGACAACTTTTTCGTGCTGGTGGTCACT 77
                                                                                                                                                                                                                                                                                                                            814 CTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACTTCTTCAATCTCGGTGGACACT
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/clone_lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                                                                                   Score 39.4; DB 17;
Pred. No. 3.1;
0; Mismatches 76;
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/clone="WHE0564_E04_E04"
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                                                                                                                                                                                                                                          390 TCTCTGAAGATAAATGTCAAGGTTGGGGGGAAGAACACTGTACTGGCTGATGCGTTGAC 449
                                                                                                                                                   558 ACCAATCGACCCCTTCAGCGACTGCAAAACCGTCGTATCGCCATCGAAGTCCGCGAGAGG 617
                                                                                                                                                                                     270 AACAATGGCTCACTTTATGGTGATCTGAAGCGTGTCTGCGAGATCGACCTTGGGCTGATT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetradoon nigroviridis

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

[ (bases 1 to 903)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurlin, W. and Weissenbach, J.
                                                                                                                                                                                                                       618 CTTCGGTCCTTACTTCCATCGTACATGATCCCATCGAACATCGTTGTTCTGGACAAGATG 677
                                                                                                                                                                                                                                                                                         678 CCTCTCAACGCCAATGGTAAAGTTGACCGGAAGGAACTCTTCTCGCAGGGCAAAGGTTGTA 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID : COAG244CD08LP1~end : T7"
t 96 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetraodon nigroviridis genome survey sequence T7 end of clone 244H15 of library G from Tetraodon nigroviridis, genomic survey
sequencing were performed in the OD Anderson lab (all
                                                                                                                      Gaps
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                                                                                    619;
                                                                                    Length
                                                                                                                    Indels
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/db_xref="taxon:99883"
                                                                                                                  94;
                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                  ىد
                                                                                                  Pred. No. 9.4;
0; Mismatches
                                157
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                                                                                  Score 37.6;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    903 bp
                         172 g
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                other authors)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-APR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL185787.1 GI:7823891
                                                                                  3.8%;
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                                                                                                               94; Conservative
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                                                                                                  Similarity
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                                                                                Query Match
Best Local S
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                                                                                  Match
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ORIGIN
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CNS028CI/c
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/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; M. truncatula sterilised seeds were germinated for
72h at 25 C, before transplanting into a 1/3 Epoisses soil:
2/3 calcined Terragreen mix in the presence of onion
root fragments colonized by the arbuscular mycorrhizal
fungus Glomus intraradices (Schenck & Smith, isolate LPAB). The plants were watered every day and twice a week with
a modified nutrient Long Ashton solution without phosphate
but with a high level of nitrate. After 3 weeks RNA was
extracted from whole root systems. cDNA was prepared from
polyA+ enriched RNA. The CDNA was directionally ligated
into Uni-zap XR vector from Stratagene and packaged using
Gigapack Gold packaging extracts. Plasmids containing cDNA
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL385769 508 bp mRNA linear EST 03-AUG-2000 MtBC30E07R1 MtBC Medicago truncatula cDNA clone MtBC30E07 T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="arbuscular mycorrhiza"
/dev_stage="harvested 3 weeks post inoculation with Glomus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inserts were mass-excised from phage stocks using Exassit helper phage and propagated in SOLR Cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of
                                                                                                                                      639
                                                                                                                                                                         Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 3132 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 508)
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
                                                                                                                                      580 FGCAAAACCGTCGTATCGCCATCGAAGTCCGCGAGGGGTTCGGTCCTTACTTCCATCGT
                                                                          Gaps
                                                                                                                                                                                                                                                                                                         640 ACATGATCCCATCGAACATCGTTGTTCTGGACAAGATGCCTCTCAACGCCA 690
                                                                      ö
   Length 903;
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Medicago truncatula ESTs from endomycorrhizal roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                      Indels
   DB 17;
                                                                      44;
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BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
                                                                   12; Mismatches
                                   26;
3.7%; Score 36.6;
49.5%; Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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79 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Genoscope
                                                                   55; Conservative
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Gaps

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256 857

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ò Db ò g ò a ð pp

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/note="Organ: uterus_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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СМ4-UT0009-050900-567-h12 UT0009 Homo sapiens CDNA, mRNA sequence.
BF094070
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Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa: Chordates; Catarrhini; Hominidae: Homo.

(bases 1 to 353)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.,Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence with grain from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-UT0009-050
900-567-hl2&t3=2000-09-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stope: 348.
                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
       tissue mRNA and cDNA amplification were performed under low stringency conditions." 102\ c \qquad 84\ g \qquad 75\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                         798 CTTTGCGAAGAAGCCACTGAGGTGTTGGCATGAAGGTTGACATTACCGATCACTTCTTC
                                                                                                                                                                                                                                                                         315 CTGGTCTATGTATTCTCCGTGGTAGACAACTCCAAAGTGGCCTTTGCCAATGACTCGGTC
                                                                                                                                                                                                                                                                                                                       858 AATCTCGGTGGACACTCTCTTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTC
                                                                                                                                 Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                              Indels
                                                                                                                                                                            68;
                                                                                                                                 DB 12;
                                                                                                                            Score 36.2; DB
Pred. No. 14;
0; Mismatches
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/db_xref="taxon:9606"
/clone_lib="UT0009"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                     918 AAGGTCCGTATCACTGTCAAGGATG 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF094070.1 GI:10899767
                                                                                                                              3.6%;
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Best Local Similarity
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MEDLINE
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1 (bases 1 to 342)

1 (bases 1 to 242)

1 (bases 1 to 242)

1 (bases 1 to 242)

1 (bases 2 to 342)

1 (bases 3 to 342)

1 (bases 3 to 342)

1 (bases 4 to 342)

1 (bases 6 to 342)

1 (bases 6 to 342)

1 (bases 7 to 342)
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-CI0132-
161100-559-g02&t3=2000-11-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 341.
Location/Qualifiers
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                                             Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 12-JAN-2001
mRNA sequence.
                                                                                                  688
                                                                                                                                           143 ACTIGCACCITACAAGATACCAACICAACTAATCGIGIGGGAGACGCICCCTCGCAATGC 202
                                                                                                                                                                                             CAATGGTAAAGTTGACCGGAAGGAACTCTCTCGCAGGGCAAAGGTTGTACCGAAGCAGCA 748
                                                                                                                                                                                                                                        203 AATGGGGAAGGTTAATAAAAAAGAGCTGAAGAAGCTGGTGACTTCAGAACAGTAAATACC 262
                                                                                                                                                                                                                                                                                         749 GACAGCAGCGCCGTTACCGACATTTCCCATCAGTGAGGTCGAAGTCATTCTTTGCGAAGA 808
                                                                                                                                                                                                                                                                                                                                         263 ATTAGAACATTATTACTGGCCAAAGCCAATTCTTTGAAACCAGTTATAATATGGTGAAA 322
                                                                                                                                                                                                                                                                                                                                                                                         809 AGCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACTTCTTCAATCTCGGTGG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                    323 ATCTTATATGACATTTGTAGTAATTATTTAGATAAAATAGAAGCCTTTTATTCTGGATTT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                             629 ACTICCATCGIACATGATCCCATCGAACATCGITGITCTGGACAAGATGCCTCTCAACGC
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     869 ACACTCTCTTGGCCACGAAGCTCATTTCTCGTATCGACCAACGACTCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
                                                     ;
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                                                  Indels
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     6
     DB
Score 36.4; DB Pred. No. 18; 0; Mismatches 1
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/db_xref="taxon:9606"
/clone_lib="CI0132"
/dev_stage="Adult"
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BF809723.1 GI:12138712
3.6%;
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LOCUS

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1. Corganism="Homo sapiens"

/ Organism="Homo sapiens"
// Organism="Homo sapiens"
// Clone_lib="NIH_MGC_40"
// Clone_lib="NIH_MGC_40"
// Lissue_type="carcinoma, cell line"
// Lissue_ty
                                                                                                                                                                                                                                                                                                                              BM048043 11near EST 07-NOV-2001
603620369F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5446001 5',
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858 AATCTCGGTGGACACTCTCTTTGGCCACGAAGCTCATTTCTCGTATCGACCACGACTC 917
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NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammallan Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapDS-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1927 row: j column: 18
High quality sequence stop: 781.
                                  798 CTTTGCGAAGAAGCCACTGAGGTGTTTGGCATGAAGGTTGACATTACCGATCACTTCTTC
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                                                                                                                        918 AAGGTCCGTATCACTGTCAAGGATG 942
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
68 a 214 c 223 g 176 t
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603622365F1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:5447729 5',
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 781)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.

Email: Gapbbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                               DB 12;
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Pred. No. 15;
0; Mismatches
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High quality sequence stop: 762.
Location/Qualifiers
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                         3.6%;
Best Local Similarity 53.1%;
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Best Local Similarity 53.1%;
Matches 77; Conservative
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                  BM044732
603622473Fl NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5447730 5',
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Directionally cloned into BcoRI/AhoI sites using the following 5' adaptor: GGGAGGAG(G) Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1932 row: b column: 19
High quality sequence stop: 786.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 792)
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                                                                                                                                                                                                                                     NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:9606"
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/clone=lib="NIH_MGC_40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
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                                                                                                 BM044732.1 GI:16773999
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                                                         mRNA sequence.
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                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arcc
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NTH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lnage.llnl.gov
Plate: LLCM1764 row: j column: 13
High quality Sequence stop: 809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: colon; Vector: porB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoNI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Strategne) and Superscript II RT (Life Technologies)" 235 c 235 g 179 t.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Eutheria; Primates; Catarrhini; Hominidae; Homo
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/tissue_type="adenocarcinoma cell li
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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Matches 77; Conservat
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 30, 2003, 12:33:15 ; Search time 115 Seconds (without alignments) 3625.576 Million cell updates/sec

1 MEYLTAVDGRQDL,PPTPASF.........RVEHLLEEVSKTFEGLNSSL 3129 US-09-482-788-2 16128 Title: Perfect score: Sequence:

Scoring table:

908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

908470

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_101002; Database

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:/ /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT: /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1982.DAT: /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1983.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT 'gcgdata/geneseq/geneseqp-embl/AA1989 'gcgdata/geneseg/genesegp-embl/AA1990 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991 /SIDS2/ /SIDS2 ١.

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995\_DAT./SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995\_DAT./SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996\_DAT./SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999\_DAT./SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999\_DAT./SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999\_DAT./SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000\_DAT./SIDS2/gcgdata/geneseq-geneseqp-emb1/AA2001\_DAT./SIDS2/gcgdata/geneseq-geneseqp-emb1/AA2001\_DAT./SIDS2/gcgdata/geneseq-geneseqp-emb1/AA2001\_DAT./SIDS2/gcgdata/geneseq-geneseqp-emb1/AA2001\_DAT. /SIDS2/gogdata/geneseg/genesegp-embl/AA1992. /SIDS2/gogdata/geneseg/genesegp-embl/AA1993. /SIDS2/gogdata/geneseg/genesegp-embl/AA1994.

Pred. No. is the number of results predicted by chance to have a scoré greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Amino acid sequenc	Mycelia sterilia c	T. niveum Cyclospo	Protein encoded by	Bacillus subtilis	Pseudomonas aerugi	Pseudomonas aerugi	Ramoplanin biosynt	Bacillus subtilis	Amino acid sequenc
QI	AAB07427	AAB73958	AAR44929	AAB07581	AAR34713	AAU36277	AAU33611	AA022159	AAR34712	AAB83971
DB	21	22	15	21	14	22	22	23	14	22
Query Match Length DB	3129	3210	15281	2841	3587	2448	4342	4999	3588	1537
Query Match	100.0	54.6	31.0	13.3	11.1	10.6	10.4	10.1	8.6	9.7
Score	16128	8199	2000	2146.5	1785.5	1713.5	1677	1632	1587.5	1572
Result No.	П	7	m	4	S.	9	7	80	6	10

ACVS. Acremonium	. epidermidis op		ത	Staphylococcus aur	Ramoplanin biosynt	Staphylococcus aur	ACV synthetase. P	ACVS. Penicillium	Protein encoded by	Escherichia coli p	sedner	Protein encoded by	Protein encoded by	Protein encoded by	Protein encoded by	cellul	Amino acid sequenc	Bacillus subtilis	S. epidermidis ope	Escherichia coli p	Escherichia coli p		Escherichia coli p	ε		a coli	. Salmonella typhi c	Human AMP-binding	Protein encoded by	Ramoplanin biosynt	Candida albicans a		C glutamicum prote
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AAR	AAG81	ABP	AAR	AAU	AAO	AAU	AAR	AAR	AAB07	ABB	AAB	AAB	AAB	AAB	AAB	AAY	AAB	AAR	AAG	ABB	ABB	AAO	ABB	AAU	AAU	ABB	AAU	AAE1	AAB07	AAO	AAY.	AAB	AAG
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## ALIGNMENTS

AAB07427 standard; Protein; 3129 AA. (first entry) 20-OCT-2000 AAB07427; AAB07427 

Cyclohexadepsipeptide synthetase; filamentous fungal cell; cyclohexadepsipeptide; antibiotic. Amino acid sequence of a cyclohexadepsipeptide synthetase.

Fusarium venenatum.

WO200042203-A2.

20-JUL-2000

13-JAN-2000; 2000WO-US00913.

990S-0229862 13-JAN-1999; (NOVO ) NOVO NORDISK BIOTECH INC.

Yoder WT; Rey MW, Berka RM,

WPI; 2000-482833/42. N-PSDB; AAA58762.

Producing a heterologous polypeptide for production of antibiotics comprises cultivating a mutant of a parent filamentous fungal cell comprising a nucleic acid sequence encoding cyclohexadepsipeptide -

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                    The present sequence represents a cyclohexadepsipeptide synthetase bolypeptide. The specification describes a method for producing a heterologous polypeptide. The method comprises cultivating a mutant of a parent filamentous fungal cell, which produces less cyclohexadepsipeptide than the parent filamentous fungal cell when cultured under the same conditions. The method if used for the production of biologically active compounds e.g. antibiotics.
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LAKKNRIISRFPSVAKVAHLSNIAFDAATWEMFAALLNGGTLVCIDYMTTLDSKTLE 1846 GGLARGYSDKALDENRFVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKI 1972 REHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDS--TAPDALDAQGLYQGV 1852 IESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVVADHDHSENDKGQSANQVE 2032 2141 HFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLHDNRSL 2092 EIGTGSGMILFNLDSRLESYVGLEPSRSAAAFVNKATESIPSLAGKAKVQVGTATD 2152 TLGKNATKDDVRQKMAELEDMEEELLVEPAFFTS-LKDRFPGLVEHVEILPKNMEA 2271 SAYRYAAVVHVRG-SLGDELVLPVEKDDWIDFQANQLNQKSLGDLL-KSSDAAIMA 2329 PIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFER RPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAV NGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELV 

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                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an enzyme which has cyclosporin synthetase-like activity. This sequence was isolated from Tolypocladium niveum (formerly known as T. inflatum GAMS). This enzyme catalyses the peptide biosynthesis of cyclosporins and structurally related molecules. This sequence may be used for the production of cyclosporin by transforming a vector containing this sequence in to a recombinant host. This allows effective production of antibiotic cyclosporin or its derivatives.
                                                                                                                                                                                                                                                                                                                                            cyclosporin
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  Enzyme, cyclosporin; synthetase-like activity; Tolypocladium n:
T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase
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SANDOZ PATENT GMBH.
SANDOZ-ERFINDUNGEN VERW GES
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93AT-0000437.
93CH-0001310.
93CH-0001375.
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N-PSDB; AAQ54386.
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Matches 1233; Conserv
                                          rolypocladium
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08-MAR-1993;
29-APR-1993;
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QY         3065GVLTKFVNIEMDEPLYDLAIAGEVEPDGAGLKVTVIAK 3102           ID         1::11   1   1 1::1::1           ID         15197 NGTNGTHANGINGSNGVNGRDSNVSAAGDQAPVHDLDIVGIPEPDGS-VKIGIGAS 15255           QY         3103 TQLFGRKRVEHLLEEVSKTFEGLN 3126           ID         1: 1   1   1: 1   1:           ID         15256 RQLLGEKVVGSMLNELCETMLALS 15279	RESULT 4 AAB07581 ID AAB07581 standard; Protein; 2841 AA. xx	AC AAB07581; XX DT 20-OCT-2000 (first entry)	Protein encod	XX XX BLM gene cluster; bleomycin gene cluster; polyketide metabolite; KW bleomycin; bleomycin analogue; bolo-carrier protein; thiazolidine; KW thiazoline; bithiazoline; microbial metabolite; sugar.			PD 13-JUL-2000. XX PF 06-JAN-2000; 2000MO-US00445.	06-JAN-1999; 05-FEB-1999;	05-JAN-2000; 20 (REGC ) UNIV CA		XX XX PT New bleomycin gene cluster components useful for peptide and/or PT polyketide metabolites, especially bleomycin, production and for		CC AAB07580-89 represent proteins encoded by open reading frames (ORFs) CC 8 to 30 of the BLM (Bleomycin) gene cluster. The proteins encoded CC by the gene cluster are useful for producing peptides and/or polyketide cC metabolites, especially bleomycin or bleomycin analogues. They are				Similarity 28.9%; Pred. No. 3.9e-163; 2; Conservative 394; Mismatches 1025; In FWQTHLNDLNASVFPHLSDHLMVPNPTTTAEHRITFPLSOK	Db 539 YWKRAL-DGAPSVLRLPMDHPRPAVQSERGETVGFALPDALVAALEKLGREQGATLF 594 Qy 284 RTALSILLSRYTHSDEALFGAVTEQSLFDFHYLADGTYQTVAPLRVHCQSNLRASD 340
14071 LDGVVDEPVLSTVSTRFDLEFHAFQEADRLNGSVMFATDLFQPETIQGFVAVVEEVLQRG 14130 2577 LQQPVS	2583 2582 14251 TPSARMEAIISSVPGRRLILVGSGVRHADINVPNAKTMLISDTVTGTDAIGTPEPLVVRP 14310	2583 2582 14311 SATSLAYVIFTSGSTGKPKGVMVEHRAIMRLVKDSNVVTHMPPATRMAHVTNIAFDVSLF 14370	1	14371 EMCATLLNGGTLVCIDYLTLLDSTMLRETFEREQVRAAIFPPALLRQCLVNMFDAIGMLE 14430 2583 2582	14431 AVYVAGDRFHSRDARATQALAGPRVYNAYGPTENAILSTIYNIDKHDPYVNGVPIGSAVS 14490	O505g	14491 NSGAIVMDKNQQLLFFGVWGEELVVTGEGVARGYTDASLDTDRFVTVTIDGGRQRAFRTGD 14550 2588 2587	RVRYRPKGFQIEFFGRLDQQAKİRGHRVELGEVEHALLSENSVTDAAVVLRTMEEEDPQL	2588 2587 14611 VAFVITDHEYRSGSSNEEEDPYATQAAGDMRKRLRSLLPYYMVPSRVIILRQMPLNANGK 14670	2588 -DRSAHMAPRIETEAILCDEFAKVLGFQVGITDNFFDLGGHSL 2629 	2630 MATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAE 2683         :  :	2684 YSPFQLLFTEDPEEFWASEIKPQLEL-QEIIQDIYPSTQMQKAFLFDHTTARPRPFVPFY 2742	IDPPETA - DCRELASACAALVOHFDIRTVFVSRGGRRYQVVLAHLDVPVFVSTEDRIL  LDFPETA - DCRELASACAALVOHFDIRTVFVSRGGRRYQVVLAHLDVPVFVSTEDRIL  LDFPETA - DCRELASACAALVOHFDIRTVFVSRGGRRYQVVLAHLDVPVFVSTEDRIL  LDFPETA - DCRELASACAALVOHFDIRTVFVSRGGRRYQVVLAHLDVPVFVSTEDREL	2803 NTATNEFLDEFAKEPVRLGHPLIRFTIIKQT-KSMRVIMRISHALYDGLSLEHVVRKLHM 2861 : :: :    ::  ::  :      14900 DEVALALHEADKQQPLRLGRAMLRIAILKRPGAKMRLVLRMSHSLYDGLSLEHIVNALHA 14959	KAL	2921 HLSKIVNIPSQVLRGSSNIITQATVFNAACALVLSRESDSKDVVFGRIVSGRQGLPVEYQ 2980	2981 DIVGPCTNAVPVRAHI-ESSDYNQLLHDIQDQYLLSLPHETIGFSDLKRNCTDWPEAITN 3039 11111	3040 FSCCITYHNFEYHPESQFEQQRVEM

1566	1314	1622	1374	1682	1434	1742	1493	1800	1553	1860	1613	1920	1673	1980	1733	2026	1787	2080	1840	2131	1894	2184	1952	2244	2012	2302	2070	2358	2130	2417	2189	2475	2249	2535	2590
qq	Qy	qa	. Oy	qq	Qy	qq	Qy	qa ·	δλ	qo,	δλ	qq	Qy	qo	ΟŸ	QQ	Qy	Dρ	ογ	qq	Oy	QQ	ΟŊ	Dp	Οy	Dp	Οy	qa	Qy	qq	Qy	qq	Οy	qo (	d d
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. 595 MTLLGAFQVLLARHAQGEDIVVGVPAAGRTRTETEPLV-GFFVNTLPLRAICAPGLSFRD 653		DLI	FMPCNNRALLLHCOMESSGA	710 GTEVERYPQEAVSQFDLSLDIKRADDGSYRGILNYCPDLFDRRRMEVLV 759	428 AYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTE 471	:  :	472 YDRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVH 531		532 IKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATV 591	:  : ::    :	592 ALTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQDLAYVIFTSGSTG 646	:	ā			SWMLAGHELFIVPEDVRRDPSALVRFVREHRIDVIDTTSSQLELLVSHGLLDGEWAP	TLVLVGEQMSSSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRAVGA-	SHYWYGGEAVSPSLWRTLRDQRRTRCFNLYGPTEATVDATCHDLS-DPADV-PVIGTP	HSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFP	:   :	DGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGORVELGAIETHL-ROOMPDDLTIV		VEATKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEOVLPRHSIPSFY	:    :    :    :  DDAHARVRRFAQGRLPAHMVPSAV	15 ICMLELPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWV 1032	SERIE SNICKLDRARLPAPAAGRPELDVRFVAPRDMVEEVVAQVMC	QSLGIDPATVNVGATFFELGGNSITAIK-MVNMARSVGMDLKVSNIYQHPTLAGISAVVK		GDPLSYTLIPKSTHEGPVEOSYSOGRIWFLDOIDVGSIWYLIPYAVRMRGPVN	AARTEGLGRGAAPPLGPVD-RSGPLPLSFAQQRLWYLDQLAPDSVSYNMCDAYRVRGPLD		:           :          ::      :  LDALRRALRTLVERHETLRTAFVERDGVPHQVVSAPDAPAARRAAEVVRIEAAGRTDEAV		:::	**************************************
59	34	65	38	71	42	16	47	80	53	84	59	06	647	954	693	1014	746	. 1071	800	1127	828	1179	915	1239	975	1280	1033	1329	1092	1387	1145	1446	1198	1506	1258
qa	QY	QQ	Qy	qq	Οy	qq	Qy	qa	Qy	qq	Qy	qa	ΟŸ	qq	ØΣ	qα	Qy	qa	Qy	QQ	δŏ	QQ	δý	QQ	Qy	qq	, <sup>X</sup> 0	qq	ά	QQ	Qy	qa	Qy	qa	Qy

14 FARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVI 1373 22 HPRPAVQSQRGETVEFPLPAPLVARLEALCREQGVTLFWALFGAFQVLLARYSGQDDVVV 1681 GTPIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERV 1433 3 TDSLKGSVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVL 1552 3 NVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPA 1612 EHV--TGDP-AGLPPLDVQYADFAVWQRSWMTGPVREEHLAYWKRAL-DGAPSVLRLPAD 1621 14 VSALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYT-RFDMEFHLFQE 1492 ETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTA 1672 3 HRVI-----IRTVTSGCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMT 1786 7 TLDARALKOVFFREHVN----AASHVTSSSQDVPL---RVPRRLSRTLMFFFLVVTDSTA 1839 | | | : | ::| | RRDPEALVALVRRAAIDVLNVTPSHLTLIEAGLLEGDRVPGT------VLVGGEAV 2130 PPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIE 1732 0 PDAL-----DAQGLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGVP-IGRALNNSGA 1893 2069 | : | ||: | || : | |||||: | |||||: || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : | RYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVÜQQNEDQAPEILG 2011 O IDFDEMHEWLGETTRTLHDNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEPSRSAAAFV 2129 NKATESIPSLAGKAKVQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYL-AEIADTLIH 2188 RDGLRRRP--AHRVRLCHREATDFTGVRAASTDLVVVNSVVQYFPDRAYLDTVLARALDA 2474 9 LPNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFF 2248 TSLKDRFPGLVEHVEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLP-VEKDDWIDFQ 2307 ANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAFERQVVASLNSNIDEWQLSTIRSSAEGD 2367 FVV -- ADHDHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQ 99 4 32 0 g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELIRSYDILRTVFVHQQLQKPRQVVLAER--KTKVHYEDISHADENRQKEHIERYKQQVQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                             operon which encodes the multienzyme complex surfactin synthetase (MCSS). Analysis of the sequence showed four regions potentially coding for proteins, a zone upstream of the first ORF contg. the srfA operon promoter and a presumed terminator positioned downstream of the stop codon of the fourth ORF. ORF2 encodes a protein (shown) which can be divided into 3 adjacent repeat regions with internal homology followed by a region (module B) of 500 mmino acids very similar to that of ORF1 and homologous to tyrocidin and gramicidin synthetase subunits I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 IQKRSALDGNLLNHLVAFENYPLDQELENGSMEDRL------GF--SIK
                                                                                                                                                                                                                                                                                                                                                                                                                113 RQAFNLAKDILFKVAVFRLAADQLYLAWSNHHIMMDGWSMGVLMKSLFQNYEALRAGRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGN
                                                                                                                                                                                                                                                                                                                                                                                          41 LDSSRIEAIKPCTPFQLDMIDCNALDKQSA----IG-HAVYDVPTDIDISRFALAWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNRFVLLEDMQTK------KCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----HLSDHLMVPNPTTTAE-HRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTEQSLPFDKHYLAD--GTYQTVAPLRVHCQSNLRASDVMDAISS----YD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 VESAF-------EQTSFDFNLIVYPGKTWTVKIKYNGAAFDSAFIERTAE---HL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRMMEAAVDQPAAFVREYGLVGDEEQRQIVEVFNSTKAELPEGMAVHQVFEEQAKRTPAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYVPLDPALPGDRLRFMAEDSSVRMVLIGNSYTGQAHQLQVP-----VLTLDIGFEESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETPESSDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLNDL-NASVFP-----
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                     DB 14; Length 3587;
                                                                  The Bacillus subtilis chromosomal DNA region comprises the srfA
                                                                                                                                                                                                                                                                                                                                                       953;
                                                                                                                                                                                                                                                                                                                                                       731; Conservative 458; Mismatches 1131; Indels
                                                                                                                                                                                                                                                                                                                   Score 1785.5; DB 1 Pred. No. 1.1e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESSHFMPCNNRALLLHCQMESSGALLVAY-----
                                 Claim 15; Page 35-42; 70pp; English.
                                                                                                                                                                                                                                                                                                                     11.18; 22.38;
pharmaceutical prods
                                                                                                                                                                                                                                             See also AAR34712-21
                                                                                                                                                                                                                                                                                  3587 AA;
                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                             SAPLTNTPTRHPSARQGGSAADGLRSWLAERLPAHLLPARITEVDALPRTGTGKLDRGAL
                                                                                                                                                        ----SRRAKVVPKQQTAAPLRTFPISEVEVILCEEATEVFGM-KVDITDHFFNLGGHS
                                              --VEPEDLWGLADSTPYRVSVSWAAA-DPRGAMDVLLVRRDAHDDGPLLVPHPVP---EP
                                                                                 SDLLTNRPLQRLQNRR---IAIEVRERLRSLLPSYMIPSNIVVLDKMPLNANGKVDRKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multi-enzyme complex surfactin synthetase DNA - is isolated from Bacillus subtilis, and used for prodn. of surfactin for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surfactin synthetase; MCSS; ORF; surfactant.
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LLAVRAVARC-RRAGVRLTVRQLLSEQTVAALAAALEE 2838
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1900..1
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3255..2
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02-SEP-1992;
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EDDPGLATLVIJAGEOMSSSVARIWAPKLOLLINGYGOSESSSICPASHWSTEP     CGSIPOPGLATL	1990 SSVRDAAVVLQQNEDQAPEILGFVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIGEI  1926 SGIQE-AVVLAVSEGGLQELCAYYTSDQD	QY         2470 PLNANGKVDRKELSRRAKVVPRQQTAAPLPTFPISEVEVILCEEATEVFGMKVDITDHFF 2529           Db         1983 PLTANGKTDRNALPKENAA
	MAEHVTEAAVIIRKNKADENEICAYFTADREVAVSELRKTLSQ VLPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQTOGAIVOQAPAPIPVFA	RUVSALOPGSRDLSSTPLAQLIFAVHSOKDLGRFKFGGLESVPVPSKAYTRFD  ::     :     :     :   :     :

to identify proteins used in proliferation, to express these proteins, conditions used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.  The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Cformat directly from WIPO at Cformat directly from WIPO at XXX Sequence 2448 AA;	Query Match 10.6%; Score 1713.5; DB 22; Length 2448; Best Local Similarity 28.6%; Pred. No. 3.8e-128; Matches 586; Conservative 327; Mismatches 750; Indels 385; Gaps 76;	QY 430 YDHNVIDSLQTTRLLQQFGHLIK-CLQSPLDLSSMAEVNLMTEYDRAE-IESWNSQPLE- 486   ::  :  :  :	OY 487 -VODTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNYSSRLAVHIKSLGLRAQQAIIP 545	QY 546 VYFEKSKWYIASMLAVLKSGNAFTLIDPNDPPARTAQVYTQTRATVALTSKLHRETVQ 603	QY 604 KLVG-RCVVVDDELLQSVSASDDFSSLTKSQDLAYVIFTSGSTGDPKGIMIEHRAF 658 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	QY 659 SSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCVCIPSDDDR 710	QY 711 MNSIPSFINRYNVNWMMATPSYMGTFSPEDVPGLATLVLVGEQMSSSVNAIW 762 :	QY 763 APKLQLLNGYGQSESSICFASNMSTEPNNMGRAVGAHSWUIDP 806	QY 807 NDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLYR 864	QY 865 TGDLARVASDGSIVCLGRIDSOVKIRGORVELGAIETHLRQQMPDDLTIVVEATKRS-QS 923   111111: 11: 11: 11: 11: 11: 11: 11: 1	QY 924 ANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRT 983	QY 984 ATGKIDRRRLRIMGKDILDKQTQGAIVQQA-PAPIPVFADTAAKLHSIWVQSLGIDPATV 1042	Qy 1043 NVGATFFELGGNSITAIKMVMAR-SVGMDLKVSNIYQHPTLAGISAVVKGDPLSYTLIP 1101 ph 1042 Gliddefflighten	1102 KSTHEGPVEQZSGRKMFLDQLDVGSLWYLIPYAVRHGPVNVDALŘRALAALEGRHET 1102 LADRQQPLALSFAQERQWFLWQLEPESAAXHIPSALRRRGRLDVDALQRSFDSLVARHET 1102 LADRQQPLALSFAQERQBRUGUEPESAAXHIPSALRRRGRLDVDALQRSFDSLVARHET	Qy 1162 LRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLS 1212
2203 APLIRAALLETEAKKHLLLDMHHIJADGVSRGIFVKELALLYKGEQLPEPTLHYK 2258 CC 2874 FSRYMQYTADGRESGHGFWRDVIQNTPMTLLSDDTV-VDGNDAT 2916 CC 2259 DFAVWQNEAGKERKEHEAYWKSULSGELPELDLPLDYARPPVQSFKGDTIRFRTGSET 2318 C2259 DFAVWQNEAGKERKEHEAYWKSULSGELPELDLPLDYARPPVQSFKGDTIRFRTGSET 2318 CC 2917 CKALHLSKIVNIPSQVLRGSSNIITQATVENAACALVLSRESDSKDVVFGRIVSGRQGLP 2976 CC 1	3036 AITNFSCCITYHNFEYHPESQFEQQRVEMGVLTKFVNIEMDEPLYDLAIAGEVEPDG 3092 ::   ::	3093 AGLKVTVIAKTQLFGRKRVEHLLEEVSKTFEGL 3125	RESULT 6 AA0136277 FINAL SANTAGORY CHANGES SANTE	6440 56.	cellular proliferation protein #267.	Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design. Pseudomonas aeruginosa.  Db	WO200170955-A2 Qy 27-SEP-2001 Db	2001WO-US09180.		2001US-26930BP. RA PHARM INC.	n KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;	4935/10. 4136. eqtides for the identification and development of			ets

δδ	SEAGWRATLERLGEDD	Qy do	2202 SQATNEHFLAARAIHTLGKN
qa	1211 RGPLLRVNLLQLAEDDHVLVLVQHHIVSDGWSMQVMVEELVQLY-AAYSQGLDVVLPA 1267	2 6	
oy d	1273 LPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSPA-KIPTDFARPALLSGDAGCVHV 1329	Д	225Z KDRFPGLVEHVETLPKNMEAVNELSAYRY :: :      :: 2226QLLQEHPEGVFNLAGW
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oy Dp	1330 TIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDII 1389 :    :::  '   :	qa	
Oy	1390 GCEVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGSRDLSSTPL 1449	RESULT	7 E. 3
QQ	1388 GFFVNTQVLKADLDGRMGFDELLAQARQRALEAQAHQDLPFEQLVEALQP-ERNASHNPL 1446	AAU33611 ID AAU	3011 AAU33611 standard; Protein; 4342 AA.
Qy	1450 AQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTRFDMEFHLFQETDSLKG 1498	X SC X	AAU33611;
qq	AWDGQTA	DT	14-FEB-2002 (first entry)
δλ	1499 SVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHVD 1558	DE	Pseudomonas aeruginosa cellular prolif
qq	1499 SFDYATDLFDASTVERLAGHWRNLLRGIVANPRQRLGELPLLDAPERRQTLSEWNPAQRE 1558	KW	Antisense; prokaryotic cellular prolifi antibiotic; antibacterial; drug design
δλ	1559 YPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAV 1618 : :   :    :    :    :	XX OS	
QQ	1559 CAVQGTLQORFEEQARQRPQAVALILDEQRLSYGELNARANRLAHCLIARGVGADVPVGL 1618	XX	
δλ	1619 FAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLI-GHDTAPPD 1675	XX	27-SEP-2001
QQ	1619 ALERSLDMLVGLLAILKAGGAYLPLDPAAPEERLAHILDD-SGVRLLLTQGHLLERLP 1675	XX	
ΟŊ	1676 IEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMI 1731		21-MAR-Z001; Z001W0-0S09180.
Db	1676 -RQAGVEVLAIDGLVLDGYAESDPLPTLSADNLAYVIYTSGSTGKPKGTLL 1725		21-MAR-2000; 2000US-191078P. 23-MAY-2000; 2000US-206848P.
Qy	SAS		23-OCT-2000; 2000US-207/27P.
qq	1726 THRNALRESATEAWF-GFDERDVWTLFHSYAFDFSVWEIFGALLYGGRLVIVPOWVSRS 1784		22-DEC-2000; 200008-253625P.
Qy	PLRVPRRLSRT		16-FEB-2001; 20010S-269308P.
qa	1785 PEDFYRLLCREGVTVLNQTPSAFKQLMAVACSADMATQQPALRYVIFGG 1833	PA XX	RA PHARM INC.
ÓΥ	1841 DALDAQGLYQGYQCYNCYGPTENGVMSTIYPIDSTESFINGVPIGRALN 1889	PI I	Haselbeck R, Ohlsen KL, Zyskind JW, Yamamoto RT, Xu HH;
qq		XX	WPI; 2001-611495/70.
Qy	1890 NSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDK-ALDENRFV-HITVNDQTVKAYRT 1947	DR	N-PSDB; AAS51470.
qq	:  ::  :    :   :	Td .	New polynucleotides for the identification antibiotics, comprise sequences of anti-
Qγ	1948 GDRVRYRIGDGLIEFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAP 2007	XX BS	Example 3; Seq ID No 5107; 511pp; Engl.
qq	1952 GDLARFQ-ADGNIEYIGRIDHQVKVRGFRIELGEIEAALAGLAGVRD-AVVLAHDGVGGT 2009	¥ 50 €	
Οy	2008 BILGFWVADHDHSENDKGQSANQVEGWQDHFESGMYSDIG 2047	388 	prokaryotic cellular proliferation, the genes, their use in the discovery of no
qq	2010 QLVGYVVADSAEDAERLRESLRESLKRHLPDYMVPAHLMLLERMPLTVNG 2059	388 ——	genes themselves and the encoded prote. Escherichia coli, Staphylococcus aureus
Qy	2048 BIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLH 2087	888 ——	pneumoniae, Pseudomonas aeruginosa and invention is also useful for the ident:
qa	2060 KLDRQALPQPDASLSQQAYRAPGSELEQRIAAIWAEILGVERVGLDD 2106		for antiblotic development. The antiser to identify proteins used in proliferal
Οy	2088 DNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEPSRSAAAFVNKATESIPSLAGKAKVQV 2147		and to obtain antibodies capable of bir The proteins can be used to screen comp
qa	2107NFFELG-GHSLLILMIKERIGDTCQATLSISQLMTHASVAE 2146	388	for homologous nucleic acids which are
Qy	2148 GTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVR 2201	388	a wide variety or organisms. The preseressential prokaryotic cellular prolifes
qa	2147 QAACIEGQARESLLVPLNGRREGSPLFMFHPSFGSVH 2183	 38	Note: The Sequence data for this patent of the printed specification, but was o

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inhibitors of genes essential to
, their use in identifying the
of novel antibiotics, the essential
roteins. The prokaryotes used are
ureus, Salmonella typhi, Klebsiella
and Enterococcus faecalis. The
dentification of potential new targets
tisense nucleic acids can also be used
feration, to express these proteins.
folinding to the expressed proteins.
compounds in rational drug discovery
acid sequence is also useful to screen
are required for cell proliferation in
resent sequence represents an
liferation protein.

atent did not form part
was obtained in electronic
(NATK-DDVRQKMAELEDMEEELLVEPAFFTSL 2251
: : | | : | |
REVPEWDDMVAEYAE------2225
                                                                                                       YAAVVHVRGSLGDELVLPVEKD----- 2301
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-----SLGGNLAMDVAARLEQRGRQVAF 2264
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918 TKRSGSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICM 977 	978 LELPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPADIPVFADTAAKLH 1028 ::	1029 SIWVQSLGIDPATVNVGAFFELGGNSITAIKMVNMAR-SVGMDLKVSNIYQHPTLAGI- 1086 11 :	1087SAVVKGDPLSYTLIPKSTHEGPVEGSYSQGRLWFLDQLDVGSLWYLIPYAVRWRGP 1142 	1143 VNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFE 1199 ::	1200VLNOEOTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDLNOLYS 1257 : :	1258 AALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSP-AKIPTDF 1314	1315 ARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIG 1374	1375 TPIANRNPELEDIIGCFVNTQCMRINIDHDTFGTLINQVKATTAAFENEDIPFERVV 1434 	1435 SALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTRFDMEF 1487	1488 HLFQETDSLKGSVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLE 1547 : ::     : ::	1548 KLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAG 1603 ::	1604 WLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSG 1661 	PTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATS ::  :  :  :  :  :  :  :  :  :  :  :  :	1713LAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETRMAHMATIAFDGAS 1766	1767 YELYSALLEGRTLVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVP 1816 :::  ::  ::  2388 ERLLAPLLCGARVVLRAQCQWGAEEICELIRAEGVSILGFTPSYGSQLAQWLESQGRQLP 2447	1817 LRVPRRLSRTLMFFFLVVTDSTAPDALDAQGLYQGVQCYNGYGPTENGVMSTIYP 1871 :	1872 IDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDK-ALDEN 1930 :	1931 RFVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDS 1990
Qy	Qy	Qy Db	Qy	Qy	QV	O <sub>Y</sub> Db	O <sub>Y</sub>	QY	OY .	QY	Qy	Qy	Qy	Qy	Qy	da .	Qy	0y
CC format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences. XX Sequence 4342 AA.	Query Match Best Local Similar. Watches 814; Con:	DIDISRFALAWKEIVNOTPALRAFAFTSDSGKT 	16	OWLDA	THLND 24	243 LNASVFPHLSDHLMVPNPTTTABHRITFP-LSQKALSNSAICRTALSILLSRYT	296HSDEALFGAVTEQSLPFDKHYLADGT-YQTVAPLRYHCQSNLRASDVMDAIS 34 277 OPFABILGEBREAFGANDI DEPONTA ACCORDI FONT FINDODDIA	347 SYDDRLGHLAPFGLRDIRNTGDRGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFM  1031 profitant bangaba	407 PCNNRALLLHCOMESSGALLVAX-YDHNVIDSLOTTRLLOOFGHLI	458 LDLSSMAEVNLMTEYDRAEIESWNSOPLEVQDTLIHHEMLKAVSHSPTKTAIQAMD-GDW	517 TYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDP 517 TYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDP 517 TYSELDNVSSRLAVHIKSHCLFAQAIIPVYFEKSKWVIASMLAVLKSGNAVUTIDPNDPV 518 TYVACGAVVUTIDPNV	577 PARTAQVVTQTRATVALTSKIHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQDLA	637 VVIETAGSTGDPRGIMIERRAFSSCALKFGASLGINSDTRALGFGTHAFGACLLEIMTTL		748 VLVGEQMSSSV-NAIWAPKLQLINGYGQSESSSICFASNMSTEPNNMGRAVGA 1391 FGGRAIDAFLANDYIOFIDAVALHUBVGORFFAINWHGGDAFDGESDICFDDIA	800 HSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDG 11440 VYCEVITARENI-II DAGILANGI GARDAI GARDENIADDEG	860 AKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIVVEA	1051

		40	3381 MSNHHILTDAMCRGIIMNDEFFTVGA
<b>අ</b> ධ .	2554 RFVPDPFAAEGGRLYRTGDLVRL-CDNGQVEYVGRIDHQVKIRGFRIELGEIEARLLEHP 2612	3 6	GRESCHGFW
ko ta	1991 SVRDAAVVLQQNEDQAPEILGEVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIG 2047	qa	
ã ò	2018 EIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLHDNRSLGNVLEIGTGSGMILF 2107	Qy	2930 SOVLRGSSNIITQATVFNAACALVLSRESDSF
qq	2649	a a	ORYQLT
Qy	2108 NLDSRLESYVGLEPSRSAAAFVNKATESIPSLA-GKAKVQVGTATDIGQVDDLHPDLVVL 2166 :  :    :	OY Db	2989 AVPVRAHIESSDYNQLLHDIQDQYLLSI   :   :   : : :   3545 SIPLRYOMPAGORCTVREWLNRLFERNLEL
අ :	HLKQQLPDYMVPAHLLPAL MONTONING MATERIAN M	δλ	
දු පු	ZIO/ NSVIQIRESSELLARILIBLENDVORIFEGDVRSOATNEEFF 2209	q <sub>Q</sub>	3604 VFENAPVEVSVLDRAQSLNAX
ζ	2210LAARAIHTLGKNATKDDVRQKMAELEDMEEELLV 2243	oy g	KVTVIAKTQLFGRKRVEHLLEEVSK
qq	2757 PRDLFQHQTVQSLAAVARHSQASQAEQGPVQGDSALTPIQHWFFDLPLARREHWNQALLL 2816	o .	3049 HLSYDQKYFEAPIVEKLLGEFKR 36/1
Qy fi	2244 EPAFFTSLKDRFPGLVEHVEILPKNME-AVNELSAYRYAAVVHVRGSLGDELV 2295 2817 OPPORTURE	REST AAO2	
ő, ő	IDFQANQLNQKSL:GDLLKSSDAAIMAVSKIPFEITAFERQVVASL	XX P	AAO22159 scandard; Frocein; 4999 AA.
qq	:     : :     : :                 : : : : : :     :	XX	03-OCT-2002 (first entry)
Qy	2349 NSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSARQWSQNGA 2399	ÇE X	Ramoplanin biosynthetic ORF 14 protein.
ପ୍ପ	2914 HHLVVDGVSWRVLLEDLQQVYRQFAEGAEPALPAKTSAFRDWAGR 2958	X X X	Ramoplanin; ramoplanin biosynthetic pathy
δλ	GRTLVNFPTDHHLRGSDLLTNRPLQ	KW	brosynthesis gene cluster, broengineering adenny no donn down the chlorinate, lipdepsipeptide.
qa ,	WQARLGGQPVEWPCDRP-QGDNREALAESVSLRLDPQRTRQ	xx os	Actinoplanes sp.
yo q	2436 RLCNRRIAIEVRERLRSLLESYMIPSNIVVLD	XX A S	WO200231155-A2.
3 8		XX 0 ;	18-APR-2002.
Z qa	SAYPLRLTPAOSPGE-SIK	A 4 ×	15-OCT-2001; 2001WO-CA01462.
Qy	⋖:	PPR	-OCT-
qa	3133	PR XX	2001; 2001US-0910813
Qy	2566 DLASVIRGGLGLQQPVSDGQGQDRSAHMAPRTETEAILCDEFAKVLGFQVGITDNFFDLG 2625	PA XX	) ECOPIA BIOSCIENCES INC.
qq	3145 DraleQplcOptGPIHDEQAPLPNELSVDGQVrg 3177	PI	Farnet CM, Zazopoulos E, Staffa A;
. Oy	2626 GHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREM 2681	DR S	WPI; 2002-435445/46. N-PSDB; AAL40781.
QO	3178 GELVLRWTYS-RERYDARTVNELAQAYLAELQALIEHCLEDGAGGL 3222	XX F	Novel isolated ramoplanin biosynthetic per
Qy	2682 AEYSPFQLLFTEDPEEFWASEI-KPQLELQEIIQDIYPSTQWQKAFLFDHTTARPR 2736	PPY	chemically modifying biological molecule polypeptide encoded by a ramoplanin blosy
qa	3223TPSDFPLAQLSQAQLDALAVPAGEIEDVYPLTPMQEGLLL-HTLLEPG 3269	PS	Claim 14; Page 169-186; 212pp; English.
ΟŸ	2737 PFVPFYIDFPSTSEPDAAGLIKACESLVNHLDIFRTVFAEASGE-LYQVVLSCLD 2790		The invention relates to an isolated rame nolunearide selected from a nolunearide selected
qq	3270 TGIYYMQDRYRIDSPLDPERFAAAWQAVVARHBALRASFVWNAGETMLQVIHKPGR 3325	388	Polypeptine selected from a polypeptine of 1-32. The isolated polypeptides are useful biological molecule that is a substrate for the contrast of the contrast
δλ	2791 LPIQVIETEDNINTATNEFLDEFAKEPVRLGHPLIRFTIIKQTKSMRVIMRISHALYDGL 2850	888	ramoplanin biosynthesis gene cluster, by molecule with the isolated polypeptide, w
3 8	ALDANGERGFULLEQFFFFTLKLGEARIW	388	modifies the biological molecule. The met biological molecule with at least two dif
Ş	ZOJI SUBNYKALDMIJNG-TKSLL	<del></del>	ramopianin Okrs 1-31. The polypeptines at biosynthesis of the antibiotic ramoplanir

: : : : : : : EHAGESGGMIVGDRYTRLDAADGARLRELA 3491 ILEMDE-----PLYDLAIAGEVEPDGAGL 3095 ALGESRPANLPTPP----RYRDYIAWLORQ 3431 -----DIVVDGNDATCKALHLSKIVNIP 2929 SLPHETIGFSDLKRNCTDWPEAITNFSCCI 3044 ramoplanin biosynthetic pathway de of open reading frames (ORF) iseful for chemically modifying a tite for a polypeptide encoded by a by contacting the biological le, where the polypeptide chemically method comprises contacting the different polypeptides encoded by as are useful for directing the anin in microorganisms. An isolated pathway polypeptide useful for e that is a substrate for a synthesis gene cluster hway polypeptide, antibiotic; ng; peptide synthetase module; ne; HPG; antibiotic precursor;

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bloengineering of antiblotic structures. An isolated polypeptide or its encoding nucleic acid sequence is useful for generating derivatives of ramoplanin, for improving production or for producing variants of other antiblotics of the peptide class. The isolated polypeptides are useful for synthesis of ramoplanin in vivo or in vitro, as an adenylation domain in conjunction with other peptide synthesise modules and allowing the incorporation of Thr into a peptide antibiotic precursor, for modifying fatty acid structure and/or enhancing fatty acid incorporation into the peptide antibiotic structure, for production of an hydroxyphenylglycine (HPG) containing peptide antibiotic, for enhancing secretion of ramoplanin or its variants and derivatives, for enhancing uptake of precursors for ramoplanin biosynthesis, for enhancing production of ramoplanin products or its variants or derivatives, to chlorinate HPG of a peptide antibiotic precursor, and for designing specific nucleotide probes and primers for identifying and isolating putative lipdepsipeptide-producing microorganisms. This sequence represents one of the ORF proteins of the ramoplanin producing Actinoplanes sp. microorganism of gene cluster comprising the ORFs is useful as a substrate for the invention. 

Sequence 4999 AA;

1233 --NSGAGADRVPGLFINTLPVRVRLGAPVGDALDGLRDQLIE-----LIAH-- 1422 --EHAPLAVAQQAANLFGRPLFTSIFNYRYARGAEPAGAALDGIRLLSARDLTNYPLAVA 1480 1104 AANIADVYPLAPLQEGIFFHHMMADRDSA---DVYVTPTVVEFDSRDRLDGFLAALOOVV 1160 DRT-----DVYRTSVV------WQGLREPVQVVWRHARLPV-----DEV 1193 ----RWLAVLRIH-------HLVQDHTALDILLEELAAYLAGRGGD---LPEPVPFRE 1277 1323 QAHLRLDGPLGRRVAAFAREHGVSPATLFHLAWARVLGTLAGRDDVVFGTVLFGRM---- 1378 445 265 477 596 313 DKHYLADGTY--QTVAPLRVHCQS-----NLRASDVMDAISSYDDRLGHLAPFGLRDIRN 365 92 NQTPALRAFAFTSDSGKTSQVILKDSFVFSWMCWSSSSSPDEVVRDEAAAAASGPRCNRF DIDSQSVSVVSMSCEDNAVSATHFWQTH-----LNDLNASVFPHLSDHLMVPNPTTTAE 1278 F------VAHTRLGVPREEHERYFAGLLGDVTETTAPYGLLDVHSGGLASA 366 TGDNGSAACDFQTVLLVTD-----GSHVNNGINGFLQQITESSHFMPCNNRALLLHCQ -----QFGHLIKCLQSPLDLSS-----MAEVNLMTEYDRAEI LRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVALTSK LHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQ---DLAYVIFTSGSTGDPKGIMI 43 SSRIEAIKPCTPFQLDMIDCNAL-DKQSAIGHAVYDVPTDID-----ISRFALAWKEIV 156 VLLEDM----QTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPESSDAT 1194 VLRDDLDPVEQLNALGTAW-----MDLS-EAPLVQAVVAA------RPGDPQ----MESSGALLVAYYDHNVID-------SLQTTRLLQ-----ES-WNSQPLEVQDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLG Indels 1000; Gaps HRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFGAVTEQSLPF -----Length 4999; tch 10.1%; Score 1632; DB 23; al Similarity 22.5%; Pred. No. 5.9e-121; 738; Conservative 417; Mismatches 1123; Local Similarity 212 1161 1234 266 1379 1423 446 478 537 1601 96 419 1660 Query Match Best Loca Matches q ò g ò g οy g αq g ò g ò g ŏ g ò g ŏ ò à ò ò

Qy	654	BHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCVCI-PSD 707
QQ	1707	FDASSFELWVPLLTGGTVV
Qy	708	DDRMNSIPSFINRYNVNWMMATPSYMGTFSPEDVPGLATLVLVGEQM-SSSVNAIW 762
qq	1758	SIDTGVLRQLIRAHELTHVHVTAGLLRVLAEDPSCFAGLTEVLTGGDVVPAEAVRRVLDA 1817
Qy	763	APKLQLLNGYGQSESSSICFASNMSTEPNNMGRAV-GAHSWVIDPNDINRLVPIGAV 818
qa	1818	rpGrrop
Qy	819	WYPANT
qq	1875	GELYIAGAGVARGYADMPGTTAERFVADPFTAGGRLYRTGDLVRHTGEGELV 1926
Qy.	879	RQQI
qq	1927	FAGRADDQVKIRGYRVEPGEVEAVLAALPGVSQAAVIVREDVPGD1973
Qy	926	STSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRTAT 985
QQ	1974	AYLVAAPETVEAARAHAEQRLPSYLVPSAFVQ
Qy	986	GKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLGIDP 1039
qa	2017	RAALPAP
οy	1040	ATVNVGATFFELGGNSITAIKMVNMARSVGMDLKVSNIYQHPTLAGISAVVKGDPLSYTL 1099
qa	2057	GRVGPDDDFFALGGHSLLALALVERLRRQGLGVSVRAVFDARTPAALTRRGDGGADDRPA 2116
Qy .	1100	IPKSTHEGPVEQSYSQCRLMFLDQLDVGSLWYLIPYAVRMRGPVNVDALRRALAALEQRH 1159
Db	2117	ERAGARPARLPLSYAQRRLWFLAQLEGPSATYNIPVALRLEGDLDRDALTAALRDVVARH 2176
Qy	1160	DPF.
Dp	2177	EVLRTVI
Qy	1218	REGEDDHILTIVMHHIISDGWSIDVERRDENQLYSAALKDSKDPLSA
qq	2235	RAVLABGDGTHVLVLVLHHIAADGWSMRPLARDLATAY-AARRRGQAPESETLPVQY 2291
Οy	1278	DFAKWQKDQFIEQEKQLNYWKKQLKDSSPAKIPTDFARPALI
qa	2292	YALWQRDLLGSDSDPASLI
Οy	1329	VIIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDI 1388
QQ	2351	:::!!! VHRSLRRVAADHGAT
Qy	1389	IGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGSRDLSSTP 1448
qa	2411	VGFFVNTLVLRTDLTGDPRLTDVLGQVRELTLRALAHQDVPFEKLVEELTP-ARSLARHP 2469
Qy	1449	LAQLIFAVHSQKDLGRFKFQGLESVPVPSKAY-TRFDMEFHLFQETDSLKGSVN 1501
qa	2470	LFQVMVTLDGGGPDGA-ELPGLAMSVVPTGAVPAKFDLDLTFTETFDAAGEPAGLRVDLI 2528
٥y	1502	NGLQSSRTPVSILPLTDG
Dp	2529	
Qy	1562	ESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAVF 1619
Db	2586	LPEITVAALVAEQCARTPGAVAVTGPDASLTYAELDERAARIARWIRRHGAGPGAAVCVL 2645
Qy	1620	LIGHD
Dp	2646	HERSAELVAVLLGVMRAGAAYVPVDPAYPAERIRFVVTDARAACVVSESASAGLVPD 2702

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GDKLLCAYYVGEGDI----SSQEMREHAA-------KDLPAYMVPAVFIQMDELPLTG 1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAVLGVLKAGAAFVPIDPDYPDQRIEYILQD-SGAKLLLKQEGISVPDSYTGDVILL--- 2663
                                                                               ETVLDMARLSRV---IERENISILMITTALFHLLVDLNPACLSTLRKIMFGGER--ASVE 1774
                                                                                                                                                                                                                                                                      ARWLPNGTIEFIGRIDHOVKIRGOAIELGEIEHOLOTHDRVQ--ESVVLAVD-----GGA 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAVHSQ--KDLGRFKFQGLESVPVPSKAYTRFDMEFHLFQETDSLKGSVNFADE----LF 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHVDYPRESSLAD 1567
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                                                                                                                                                                                               VFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAVFAPRSCETI 1627
                                               ----DDDRMNSIPSFINRYNVWMMATPS---YMGTFSPEDVPGLATLVLVGEQMSSSVN
                                                                                                                                                                                                                                          ARYASDGSIVCLGRIDSQVKIRGQRVELGAIE----THLRQQMPDDLTIVVEATKRSQSA
                                                                                                                                                                                                                                                                                                       NSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRTA
                                                                                                                                                                                                                                                                                                                                                                                       --ISPAEKQDIYPVSSPQKRMYVLQQLEDAQISYNMPAVLRLTGELDVERLNSVMQQLMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GA--TFFELGGNSITAIKMVNMA-RSVGMDLKVSNIYQHPTLAGISAVV----KGDPLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKADALRRLAKETDSTLYMVLLASYSAFLSKICGQDDIIVGSPVAGRSQADVSRVIGMFV
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                                                                                                                                          HVRKALQTVGKGKLLHMYGPSESTVLATYHPVDELEEHTLSVPIGKPVSNTEVYILDRT-
                                                                                                                                                                           INRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLYRTGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 LSLE-AGEGRTAAVLCERSMDMIVSILAVLKSGSAYVPIDPEHPIQRMQHFFRDSGAKVL 1604
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                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                 these regions. At the C terminal end of module 3 there is a region (module A) of 500 amino acids which has no homology with modules 1-3. Although ORFI codes for a protein of unknown function, regions of the protein are found to be highly homlogous to synthetases coded by Tych and GrsA (tyrocidin and gramicidin synthetase subunits I) and with aminoadipyl cystein valine synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPFEWLVEDLNIPRDVSRHPLFDTMFSLQNATEGIPAVGDLSLSVQETN--FKIAKFDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRHMLLFDMH-------GLPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNPTTTA------EHRITFPLSQKALSNSA----ICRTALSILLSRYTHSDEALFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVTEQSLPFDKHYLADGTYQTVAPLRVHCQSNLRASD------VMDAISSYDDRLGHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APF-GLRDIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHCQMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGG-CVCIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRFVLLEDMQTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPESSDATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDSQSVSVVSMSCEDDNAVSATHFWQT--------HLNDLNASVFP---HLSDHLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LRLQYKDYAV-----WQSRHAAEGYKKDQAYWKEVFAGELPVLQLLSDY---
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                                                                                                                                                                                                                 The Bacillus subtilis chromosomal DNA region comprises the srfA operon which encodes the multienzyme complex surfactin synthetase (MCSS). Analysis of the sequence showed four regions potentially coding for proteins, a zone upstream of the first ORF contg. the srfA operon promoter and a presumed terminator positioned downstream of the stop codon of the fourth ORF. ORFI encodes a protein (shown) which can be divided into 3 adjacent repeat regions with an internal homology of ca. 1000 bases, more marked in the second half of these regions. At the C terminal end of module 3 there is a region
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9.8%; Score 1587.5; DB 14;
Best Local Similarity 25.6%; Pred. No. 1.3e-117;
Matches 618; Conservative 405; Mismatches 957; In
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                                  Be
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 (ENIE ) ENIRICERCHE
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                                                                                                                           Multi-enzyme
                                               Rodriguez F;
                               Carrera P,
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----DGSRTILSLPLDENDEENPETAVTAENLAYMIYTSGTTGQPKGVMVEHH 2715
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                                              1735 VIIRTVTSGCIPNY----PSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLD 1789
                                                                                                                                               1790 ARALKDVF------FREHVNAASHVTSSSQDVPLRVPRLSRTLMFFFL, 1832
                                                                                                                                                                                                                                                                                                 -----NNYGPTENTVVATSAEIHPEEGSLS---IGRAIANTR 2860
                                                                                                                                                                                                                                                                                                                                                                                                                                              1948 GDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAP 2007
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                                                                                                                                                                                             2772 IVRLNDYFETNGVIITFLPTOLAEQFMELENTSLRVLLTGGD-----KLKRAVKKPYT
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                                                                                                                                                                                                                                                                                                                                             1893 AYVVDPEQQLVGIGVMGELVVTGDGLARGYSDKALDE--NRFVHITVNDQTV---KAYRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a method for the preparation; of a collection of nucleic acids from organisms in a soil sample. The method comprises milling a dried sample to produce microparticles; suspending these in liquid buffer; extraction of nucleic acids from the microparticle; passing nucleic acid-containing solution through a molecular sieve; passing nucleic acid-enriched fractions through an anion exchange chromatography material; and recovering fractions containing purified nucleic acids. The nucleic acids are sources for sequences that encode either operons involved in a metabolic pathway (specifically polyketide synthesis) or polypeptides, particularly for production of therapeutic or agricultural compounds, especially polyketide antibiotics. AABB3971-76 represent type I polyketide synthases encoded by cosmid a2691.
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DPQALRRSLQDLVDRHPALRTTIAESGGAPVQTVHSSVPVDFEVIP-CSPD-DEAVLIDG
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Ball M, Sezonov G, Tuphile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collection of nucleic acids from environmental samples, useful for identifying e.g. genes encoding polyketide synthases and derived antibiotics
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ilarity 29.3%; Pred. No. 4.8e-117;
Conservative 268; Mismatches 670;
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                                                                                                                                                                                                                                                             Guerineau M,
Raynal A,
                                                                 29-NOV-1999; 99FR-0015032
07-JUN-2000; 2000US-0209800
27-NOV-2000; 2000WO-FR03311
                                                                                                                                                                                                                                                     Jeannin P, Pernodet J, Gu
Cappellano C, Francou F,
Frostegard A;
                                                                                                                                                                                    (AVET ) AVENTIS PHARMA SA
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N-PSDB; AAF90034
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Protein; 3639
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N-PSDB; AAQ48231.
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                GL 2575
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GV 1505
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                                                                                                     AAR40227;
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EKLDVL---NVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAG
                                      WLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPT
                                                                           IVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKP----SATSLAYVLYT
                                                                                                                     -----NVTESEVWTQPDTNPNPLATPADLAYVLYT
                                                                                                                                         SGSTGRPKGVMIEHRVIIRTVTS-GCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRT
                                                                                                                                                                              LVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVPLRVP------RRLS
                                                                                                                                                                                                VVVANQETAVDGERL-----ARELARSKATMMQATPATWRLLLASGWPGDRRLT
                                                                                                                                                                                                                               GRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDK-ALDENRFVHITVNDQTVK
                                                                                                                                                                                                                                                                      AYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNE
                                                                                                                                                                                                                                                                                                        DQAPEILGFVV-----AD--HDHSENDKGQSANQVEGWQDHFESGMYSDIGEID
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1444 GEVLGMDGIGVHDHFFDSGGHSLLVTQMIARVRDMLHVEVPFRTVFNAPTVRGFAVAIQD 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coding delta-(L-alpha-amino-adipyl) L-cystinyl D-valine
.hase - for improved productivity of cephalosporin antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta-(L-alpha-aminoadipyl)-L-cystinyl-D-valine synthase; ACVS; beta-lactam; antibiotic; transförmed; cephalosporin; vector.
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Db 2054 LDAFYAV	Qy 1310 IPTDFAR	Db, 2112 LVPDRPF	Oy 1370 DAVIGTE	2172	1430	2231	1483	2284	1542	2344	Qy 1601 LAGWLRR	TO#7		2461		Db 2518 TSGTTGF	1775	2577	1834	2631	1890		1942	Db 2744 QRLYKTG	Qy 2002 NED 200.	Db 2803 DED 280	RESULT 12	AAR13896 ID AAR13896 standare	AC AAR13896;	XX DT 22-NOV-1991 (file	DE ACV synthetase.	KW Beta lactam antil	OS Acremonium chryso	FH Key	
:   :   :   :   :   :		1110 PGIERSVGLFINTLPMIFDHTVCQDMTALEAIEHVQGQVNAMNSRGNVELGRMSKN 1165	SHFMPCNNRALLLHC	1166 DLKHGLFDTLFVLENYPNLDTEQREKHEEKLKFTIKGGTEKLSYPLAVIAQE 1217	418 QMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEY 472	1218 DGDSGCSFTLCYAGELFTDESIQALLDTVRDTLSDILGNIHAPIRNMEYLSSN 1270	473 DRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHI 532	1271 QTAQLDKWNATAFEYPNTTLHAMFESEAQQKPDKVAVVYEDIRLTYRELNSRANALAFYL 1330	533 KSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVA 592	1331 LSQAAIQPNKLVGLIMDKSEHMITSILAVWKTGGAYVPIDPRYPDQRIQYILEDTAALAV 1390		1391 ITDSPHIDRLRSITNNRLPVIQSDFALQLPPSPVHPVSNCKPSDLAYIMYTSGTTGNPKG 1450	651 IMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTLINGGCVCIP 705	1451 VMVEHHGVVNLCVSLCRL-FGLRNTDDEVILSFSNYVFDHFVEQMTDALLNGQTLVVL 1507	706 SDDDRMNSIPSFINRYNVNWMATPSYMGTFSPEDV-PGLATLVLVGEOMSSSVNAIW 762	1508 NDEMRGDKERLYRYIETNRVTYLSGTPSVISMYEFDRFRDHLRRVDCVGEAFSEPV 1563	763 APKLQLLNGYGQSESSSICFASNMSTEPNNMGRAVGAHSWVIDPNDINR 811	1564 FDKIRETFPGLIINGYGPTEVSITTHKRPYPFPERRTDKSIGCQLDNSTSYVLNDDMK 1621	812 LVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLY 863	1622 RVPIGAVGELYLGGDGVARGYHNRPDLTADRFPANPFQTEQERLEGRNARLY 1673	864 RTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIVVEATK 919	1674 KTGDLVRWIHNANGDGEIEYLGRNDFQVKIRGQRIELGEIEAVL-SSYPGIKQSVVLAKD 1732	SSYFGNRPSDAHILDHDAT		980 LPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLGIDP 1039		1040 ATVNVGATFFELGGNSITAIKMVNMA-RSVGMDLKVSNIYQHPTLAGIS 1087	1828 DRISIYSDFFSLGGDSLKSTKLSFAATRALGVAVSVRNLFSHPTIEALSQWIIRĞSNEVK 1887	1088AVVKGD-PLSYTLIPKSTHEGPVEQSYSQGRLWFLDQLDVGSLWYLIPYAVRM 1139	1888 DVAVVKGGASLDIPLSPAQERLMFIHEFGHSGEDTGAYNVPLQLQL 1933	1140 RGPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQ-IVHEKLSEEMKVIDLCGSD 1194	1934 HHDVCLESLEKALRDVVSRHEALRTLITRTQKSSVHCQKILDAEEAQKLFSVDVLRLTSE 1993		1994 TEMQGRWAESTAHAFKLDEELPIHVRLYQVVRDGRTLSFASIVCHHLAFDAWSWDVFQRD 2053	1252 LNQLYSAALKDSKDPLSALTPLPIQYSDFA-KWQKDQFIEQEKQL-NYWKKQLKDSSPAK 1309
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VLADYWLRKLSDMEASY 211:	VLLAAFRAAHYRLTAVE 1369	VAAAXFLLLYVYTNOR 2171	NOVKATTTAAFENEDIP 1429	:   :: :  \AVQKELVDAQIHQDLP 2230	-AVHSQKDLGRFKFQGLESVPVPSKAYTR 148	(PPSPLPSAAK 228	GLOSSRTPVSILPLTD 1541	AHNKASTSLSKLSVED 2343	SSCRLTYTEL-DROSDI 1600	STRSLSYSELNERANOL 2400	VRSPSARVODILSGLS 1660	:       PTYPSQRTELILEESS 2460	HDSTKPSATSLAYVLY 1718	:         :: TSTQKPSDLAYVIF 2517	TIAFDGASYEIYSALL 177	NYVFDFSLEQLCLSVL 257	RVPRRLSRTLMFFFLV 183	:   RLPHLHMVTAA 263	FINGVPIGRALN 188	FKGDAPFTKALCHGIP 268:	VHITVNDOT 1941	: : IPNPEYEPKQASDSRP 274:	LLRDSSVRDAAVVLQQ 2001	:   : ::   : .VLAISAVKEAAVIPKY 2802										
AAANLPTLRVQYKEYAIEHRRALRAEQHRVLADYWLRKLSDMEASY	DFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVE	LVPDRPPRPAQFDYTGNDLQFSTTPETTAQLKELAKREGSSLYTVVAAAYFLLLLYVYTNQR	DAVIGTPIANRNPELEDIIGCEVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIP		TPLAQLIFAVHSQKDLGRF  	FQETTKLLHV-QHDPSRHPLLQAVFNWENVPANVHEEQLLQEYKPPSPLPSAAK	FDMEFHLEQETDSLKGSVNFADELFKMETVENVVRVFFFEILRN-GLQSSRTPVSILPLTD	FDLNVTVKESVNSLNVNFNYPTSLFEEETVQGFMETFHLLLRQLAHNKASTSLSKLSVED	GIVTLEKLDVLNVKHVDYPRESSLÄDVFQTQVSAYPDSLAVVDSSCRLTYTEL-DRQSDI	GVLNPEPTWLQPSSRDSGNSLHGLFEDIVASTPDRIAIADGTRSLSYSELNERANQL	VFAPRSCETIVAFFGVLKANLAYLPLI	: : : : : : : : : : : : : : : : : : :	GPTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLY		TSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETRMAHMATIAFDGASYEIYSALL	TSGTTGKPKGVLVEHQSVVQ-LRNSLIERYFGETNGSHAVLFLSNYVFDFSLEQLCLSVL	FGRTLVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVPL-RVPRRLSRTLMFFFLV	GGNKLI-IPPEEGLTHEAFYDIGRREKLSYLSGTPSVLQQIELSRLPHLHMVTAA	VTDSTAPDALDAGGLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGRALN	S-QINNAYGITETTVYNIITT	/MGELVVTGDGLARGY - SDKALDENRE	GSHVYVLNDRLQRVPFNAVGELYLGGDCLARGYLNQDALTNERFIPNPFYEPKQASDSRP	LEFFGRMDTOFKIRGNRIESAELEAP	:				3712 AA.				penicillin.		alifiers
4 LDAFYAVHTKHK	IPT :																									3 DED 2805		6 standard; Protein;		1991 (first entry)	synthetase.	Beta lactam antibiotics; pe	Acremonium chrysogenum.	Location/Qualifie 3011068
Db 205	Qy 1310	Db, 2112	Oy 1370	Db 2172		Db 2231	Qy 1483	Db 2284	Qy 1542	Db 2344	Qy 1601	Db 2401	Qy 1661	Db 2461	Qy 1719	Db 2518	Qy 1775	Db 2577	Qy 1834	Db 2631	Qy 1890	Db 2684	Qy 1942	Db 2744	QY 2002	Db 280;	RESULT 12 AAR13896	ID AAR13896	AAR13896;	22-NOV-1991	ACV		AA OS Acremoni XX	FH Key FT Domain

Region (7.4 being subdomain (7	SO Sequence 3712 AA;		Ouery Match 9.4%: Score 1515; DB 12; Length 3712; Best Local Similarity 26.1%; Pred. No. 1e-111; Matches 564; Conservative 377; Mismatches 912; Indels 310; Gaps	Qy 2 EYLTAVDGRQDLPPTPASFCSHGDSPLNSSYEQLFHLYGLDSSRIEAIKPCTPF	Db 866 KYTKASNGTNGTAHVNGHAANGHVSDSYVASSLQQGFVYHSLKNELSE	S6 QLDMID	918	QY 116 VILKDSFVFSMACWSSSSSPDEVVRREAAAASGPRCNRFVLLEDMQTKK	166	1022 YSCLFSCHHAILDGWSLPLLFNNVHQAYLDLVBGTASPVEQDATYLLGQQY	높	Db 1078DDHLDFWAEQIGRIEERCDMNALLNEASRYKVP-LADYDQVREQRQ	Qy 266 HRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFG-AVTEQSLPF	DD 1123 QTISLPWNNSMDAGVREELSSRGITLHSILQTVWHLVLHSYGGGTHTITGTTISGRHLPP	Qy 313 DKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISSYDDRLGHLAPFGLRDIRNTGDN :   :   :   :   :   :	Db 1183 PGIERSVGLFINTLPMIFDHTVCQDMTALBAIEHVQGQVNAMNSRGNVELGRMSKN	QY 370 GSAACDEQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRALLLHC     :::   :::     :::     :::     :::     :::   :::     :::   :::     :::   ::	418 OMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSM	1291	QY 473 DRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTALQAWDGDWTYSGLDNVSSRLAVHI	Qy 533 KSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVA	Db 1404 LSQAAIQPNKLVGLIMDKSEHMITSILAVWKTGGAYVPIDPRYPDQRIQYILEDTAALAV	QY 593 LTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQDLAYVIFTSGSTGDPKG	Qy 651 IMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCVCIP :	Qy 706 SDDDRMASIPSFINRYNVNMMMATPSYMGTFSPEDV-PGLATLVLVGEOMSSSVNAIW	Db 1581 NDEMRGDKERLYRYIETNRYTYLSGTPSVISMYEFDRFRDHLRRVDCVGEAFSEPV  Qy 763 APKLQLLNGYGQSESSICFASNMSTEPNNMGRAVGAHSWVIDPNDINR		RTGDLARYASDGSIVCLGRID
Region C2-TEB-1991 C3-FEB-1990 C3-CT-1990 C4-TEB-1991 C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP45868-A. C1-EP458-C1-EP458-C1-EP45		main	bdomain	subdomain	subdomain 54	ion of amino acid	subdomain 590	1= subdomain :178 1= subdomain	. 1846 el= subdomain		ction= activation of amino acid2603	abel= subdomain	adel= Suodomain 27281. 28bel= subdomain	8992928 1992928 19692938	ander subdomain 1560. 364 void 1abel = IV	L				OBP-0200475. 0BP-0200488. OBP-0201768.	OCADES NV.	, Garcia BD, Guttierez S, hren H, Palissa H, Van Liem		n used	); 54pp; English.	was obtd. from five subclones isolated from a A. chrysogenum C10 (ATCC 48). The protein uced from the DNA. Three distinct regions of en identified, domains I, II and III. Within veral even more conserved elements can be	Since the enzyme synthesises a tripeptide, which quires the activation of three amino acids, a omains in the activation reactions seems likely. Is thought to act as a thioesterase.	used to express the synthetase enzyme which can prodn. of new beta-lactam antibiotics.

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1942 VKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQ 2001
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                                                                                                                 HHDVCLESLEKALRDVVSRHEALRTLITRTQKSSVHCQKILDAEEAQKLFSVDVLRLTSE
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                                                       LPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLGIDP
                                                                              ----IVPPRTEVERILAGIWSELLEIPV
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                                                                                                                                                                                            RGPVNVDALRRALAALEQRHETLRT - - TFEDQDGVGVQ - IVHEKLSEEMKVIDL - - CGSD
                                                                                                                                                                                                                                          1195 LDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHIL ---TIVMHHIISDGWSIDVLRRD
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                                                                                                                                                                       1961 DVAVVKGGASLDIPLSP-----AQERLMFIHEFGHSGEDTGA--YNVPLQLQL
                                                                                                                                                                                                                                                                                                      1890 NSGAYVVDPEQQLVGIGVMGELVVTGDGLARGY-SDKALDENRFV------HITVNDQT
                                                                                                  1040 ATVNVGATFFELGGNSITAIKMVNMA-RSVGMDLKVSNIYQHPTLAGIS----
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used in vaccination. The nucleic acids (I) may be used to produce the separation of the manifold and the produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH5509 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present finention specifically claims all the polynucleotide sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4455 to 4472, no sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
                                     2875
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polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermidis open reading frame protein sequence SEQ ID NO:760
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NLRDFF50	IALVDVIFQORVLSRVEAAYKHEK- 197 		PITTAEHRITFPLSQRALSNSAIGRTALSILLSRYTHSD 298		FDKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISSYDD 350 	.VTDGSHVNNGINGFLQQITESSHF 405	NVIDSLQTTRLLQQF-GHLIKC 453	5 4	PVYFEKSKWVIASMLAVLKSGNAF 568 :    -	62	ALKFGASLGINSDTRALQFGTHAF 685 : :   :               -UVHNPNYVELNENTTVLLSGTVAF 587	NRYNVNWMMATPSYMGTFSPEDVPG 743	IGYGOSESSICFASNMSTEPNNMG 794	:ESPGIARDYIVPPPPEKSP 842  : : :  :  :  :  :  :  :  :  :  :  :  :	DGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETH 902    :	FGNRPSDAHILDHDATKAINIKLE 962	KDILDKGTQGAIVQQAPAPIPVFAD 1022	ILMVN-MARSVGMDLKVSNIYQHP 1081	OGRLWPLDQLDVGSLWYLIPYAVR 1138
 10 DIELRRLMYALLDVVQSQPVLRT-QFVTDDFNQLKINLRDF	141 DEAAAAASGPRCNRFVLLEDM - QTKKCQLVWTFSHALVDVTFOQRVLSRVFAAYKHEK	DIHRP	HLSDHLMVPN	SKHFNVLNADGDNYAYIPVKNTSEKKK	TEQSLPFDKHYLADG   :   	SHL	406 MPCNNRALLLHCQMESSGALLVAYYDH	454 LQSPLDLSSMAEVNLMTEYDRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTA  :	509 IQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAF 		629LTKSQDLAYVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAF 	CVCIPSDDDR :       RLVITSKDTL	744 LATLVLVGEQMSSSVNAIWAPKLQLLNGYGQSESSSICFASNNSTEPNNMG   :  :  :  :  :  :	795 RAVGAHSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSP :     :    :    :	YPANTEP	903 LRQQMPDDLTIVVEATKRSGSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLE	963 QVLPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKGTQGAIVQQAPAPIPVFAD 	1023 TAAKLHSIWVQSLGIDPATVNVGATFFELGGNSITAIKMVN-MARSVGMDLKVSNIYQHP :  :	1082 TLAGISAVVKGDPLSYTLIPKSTHEGPVEGSYSGGRLWFLDQLDVGSLWYLIPYAVR 1: :   :

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1012 LSSELNVWQLQRALSKLIERHEILRTQYVIDDNEVKQRIATHVSPDFEEVT---TSLTNE 1068 MRGPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPF 1198 EVLNQEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDLNQLYSA 1258 SINGSFMEPFDLEQPSQMRVKYIHGPQQDY-LFMDTHHSINDGMSNTILLSDLNALYQD 1127 ALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSP-AKIPTDFARP 1317 1438 QPGSRDLSSTPLAQLIFAV-HSQKDLGRFKFQGLESVPVPSKAYTRFDMEFHLFQETDSL 1496 1297 -VDERDASHNPLFDVMLVLQNNETNHANFGHSQLTHIP-PQSTTAKFDLSFIIEEDQDDY 1354 1497 KGSVNFADELFKMETVENVVRVFFEILRNGLØSSRTPVSILPLTDGIVTLEKLDVLNVKH 1556 V-----DYPRESSLADVPQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMP 1611 APPDIEVTNVEFVRIRDALNDSNADGFEV----IEHDSTKPSATSLAYVLYTSGSTGRP 1726 1727 KGVMIEHRVIIRTVTSGCI----PNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCV 1782 1783 DYMTTLDARALKDVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFL--VVTDSTAP 1840 1841 DALDAQGLYQGVQCY-NGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPE 1899 1679 TPAFVQHISKHCDMYVNAYGPSENTVITSCWIYEKGDAIPSTIPIGKPLANVDIFIMS-G 1737 1900 QQLVGIGVMGELVVTGDGLARGYSDK-ALDENRFVHITVNDQTVKAYRTGDRVRYRIGDG 1958 1903 KFVAPRN-NIEREIAQIV-----SGVLDVSSMSIDD-------DFFEMGGTS 1941 1318 ALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPI 1377 1378 ANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSAL 1437 1612 AETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDT 1671 2019 HSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEW 2078 LGETTRTLHDNRSLGNVLEIGTGSGMI -- - LFNLDSRLESYVGLEPSRSAAAFVNKATES 2135 2136 IPSLAGKAKVQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAE-----IADTLI- 2187 1139 1199 1069 1259 1128 1557 1672 1529 2079 Oy Oy Ob Oy Oy Dp 07 07 g Óγ QQ Oy Oy Ob oy Oy Ω οŽ QQ ò

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946 AHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQT 1005
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                                                                      QSAIGHAV - - - YDVPTDIDISRFALAWKEIVNQTPALRAFAFTSDSGKTSQVILKDSFVF
                                                                                                                183 QRVLSRVFAAYKHEK-----DTHRPETPESSDATDTDSQSVSVVSMSCEDNAVSATHFW
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       Conservative 466; Mismatches 1032;
   582;
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       2223
                                                                                                                                                                                                         2096
                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP315124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                2281 AAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAF
                                                                   DHLPQLQSLV--ERRYQLKSQHLTQSSLGHVLLTGATGFLGAYLIDEMQDDADQITCIVR
                                                                                                                                      KDDVRQKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNEL---SAYRY
                                                                                                                                                                                                                                                                                                                                                                                                           ERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSARQWSQNGAL
                                                                                                                                                                                                                                                                                                                         2097 DTIIHA-GARTDHF-----GDDETFFDVNVRSTQALIDLAKDKKAKLIYISTI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2404;
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Pred. No. 8.4e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAVFHHCCSQGRTLVNF -- PTDHHLRGSDLLTNR 2432
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Best Local Similarity
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08-NOV-1997;
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Similarity 25.9%; Pred. No. 1.8e-103; 96; Conservative 320; Mismatches 812; Indels 287; Gaps	AEHRIT	-	<ul> <li>-VTEQSLPFDKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISSYDDRLGHLAPFGLRDI</li> <li>:: : : : : : : : : : : : : : : : : : :</li></ul>	RNTGDNGSAACDFQTVLLVTDGSHVNNGING		SSGALLVAYYOHNVIDSLQTTRLLQQFGHLIKCLQSP   :   :         :   :         :			TYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDP 				TDLAYAIYTSGTTGRPKAVLIEHRGVVNLHTSLERLFDLSRD-RGDEAVLSFSNYVFDHF		VEQMTDALLSGQTLVMLDDSMRSDQQRLYAX	LVLVGEQMSSSVNA: :	IDAIGEDFTTPVFDKIRSSFGGLI			PANTFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDL		TIVVEATKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPR : :   :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : : :   : : : : :   : : : : :   : : : : : : :   :	Ξ	VPVRIIRILEIPVTGSGKLDVKRLPATEFALAGSVDYVQPANQTERDL		CRLWSKVTGLGPDRIGSRDDFFGSGGDSLRAIKLAQSITAHFGQNFNVAAVFAHFNIAAQ		æ	RGPVNVDALRRALAALEQRHETLRTTFED-QDGVGVQIVHEKLSEEMKVIDLCGSDL 	DPFEVLNGEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLR
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qq	7	PDRSALDAELVADFAHVFRLDQELPLRARLFAVGSDRRSIVVSLVFHHSCFDGWSWRIFR 21
Qy	1250 2133	RDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSP 1307
Qy	1308	AKIPTDFARPALLSGDAGCVHVTIDGELYOSLRAFCNEHNTTSFVVLLAAFRAAHYRLTA 1367 
Οy	1368	
Db	2247	
Qy	1428	IPFERVVSALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKF
Db	2307	
Qy	1473	VPVPS
q <sub>Q</sub>	2358	TTAKFDLSATVSETAQGLSVNFTYAASLFDASSVDNIVATYRRILQEFCR 2407
Qγ	1533	PVSILPLTDGIVTLE
qq	2408	LAPMAESAALSDIRYVEACAAPAPAAIAEERAAETLH
Qy	1584	DSSCRLTYTELDROSDILA-GWLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLP 1642
qa	2462	FGDTRLSYRELDARANRLARSLLASRTLAPGDFVALVLDKSEWTVVALLAVWKAGAAYVP 2521
Oy	1643	LDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALN 1691
qq	2522	IDPGYPDERIAFWLEDTGARAVIADEASYPRISALAGHAARPVLNVHA 2569
Qy	1692	
qq	2570	
Qy	1752	
QQ	2629	AGAARQAILFLSSYVFDFSVEQLALSILSGNALLIPESSLLFDDAFYQRMNQERL 2683
Qy	1806	SHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALD-AQGLYQGVQCYNGYGPTENG 1864
qq	2684	SYISGTPTQLQLFDLARLDHLHAVLVAGEAFRAHHFDKIRAEYRG-PLYNAYGTTE 2738
٥y	1865	VMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLAR 1920
Db	2739	TTVYNLVRRFAPDAPYRNDLGHAIANTELHILDGELRELPPGGLGEIYMAGDCVGA 2794
Οy	1921	QTVKAYRTGDRVRYRIGDGL
Db	2795	GYLNRDELSRERFVANPFRSEDDRRLGRNDTLYKTGDLVRRR-HSGELEFFGRNDHQ 2850
Οy	1970	FKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVVADHDHSEN 2022
qa	2851	VKINGVRIELGEIEAVAAAFPGVAQCAVVARHDGERSGGSRLVCYYVAAHNVSES 2905

Search completed: May 30, 2003, 12:44:23 Job time : 162 secs

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2488.225 Million cell updates/sec
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5.1.6
Compugen Ltd.
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Description		Sequence 2, Appli	80,	93,	Sequence 4, Appli	13,	25,	3464	۲	27,	2, 4	12,	33,	3, 2	'n	'n	'n	ω,	Sequence 3, Appli	'n	σì	91,	81,	5,	8	9	28,	
SUMMARIES		US-08-471-119A-2	-814-8	US-09-413-814-93	US-08-222-617A-4	US-08-222-617A-13	US-08-222-617A-25	US-09-134-001C-3464	US-09-413-814-11	US-08-222-617A-27	US-08-222-617A-2	US-08-222-617A-12	US-08-510-646B-33	US-09-335-409-3	US-09-568-102-3	US-09-567-969-3	US-09-568-480-3	US-09-568-486-3	US-09-568-472-3	US-09-567-899-3	US-08-222-617A-9	US-09-413-814-91	-09 - 413	US-08-222-617A-5	US-08-222-617A-8	US-08-222-617A-6	US-09-413-814-28	US-08-222-617A-7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,119A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435

TITLE OF INVENTION: Cyclosporin Synthetase NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:

Sequence 2, Application US/08471119A Patent No. 5827706 GENERAL INFORMATION:

JS-08-471-119A-2

APPLICANT: Leitner, Ernst APPLICANT: Schneider, Elisabeth APPLICANT: Schoergendorfer, Kurt APPLICANT: Weber, Gerhard

5: No. 5827706artis Corporation 59 Route 10

ADDRESSEE:

STREET:

East Hanover: New Jersey

USA

STATE: No

07936

100-8029/CONT/CONT

NAME: Kassenoff, Melvyn REGISTRATION NUMBER: 26,389 REFERENCE/DOCKET NUMBER: 100

ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION: TELEPHONE: 201 503 8474 TELEFAX: 201 503 8807

TELEFAX: 201 503 8807 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

15281 amino acids

LENGTH:

STRANDEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO

amino acid

DB 2; Length 15281;

Score 5000; Pred. No. 0;

31.0%;

Query Match Best Local Similarity

ORGANISM: Tolypocladium niveum STRAIN: ATCC 34921

ANTI-SENSE: NO ORIGINAL SOURCE:

520.5	 	514	4 -	US-09-413-814-82	Sequence	82, Appl
		2520	4.	US-09-413-814-94	Sequence	4,0
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۲.	2.7	515	4	US-09-413-814-22		22,
٤.	5.6	401	4	US-08-861-774E-88		88
93	2.4	489	4	US-09-134-001C-4902	Sequence	4902
٦.	2.4	399	4	US-08-861-774E-86	Sequence	86,
77	2.3	390	4	US-08-861-774E-82		82,
9/	2.3	392	4	US-08-861-774E-24		24,
369	2.3	388	4	US-08-861-774E-94		94,
5.	2.3	390	4	US-08-861-774E-18		18,
352.5	2.2	396	4	US-08-861-774E-84	Sequence	84,
'n	2.5	392	4	US-08-861-774E-92	Sequence	92,

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66; 541 11639	595	11699	653 11754	702	11806	759	810	11922	-c+ (	89611	922 12028	365	12078	1025	12125	1080	140	12244	1200	12303	1260	12303	1318 12422	1378	12482	38	12542	1498
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12722 12937 13056 13115 1616 1676 FFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDA-QGLYQG---- 1851 13294 GTRMDRQALLQLLQDRQRGDDVVAVSNIPYSKTIMERHLSQSLDDDEDGTSAVDGTAW-I 13473 1897 2017 2077 2135 1957 2307 2136 IPSLAGKAKVQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRI 2195 2357 STIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSARQWSQNGALDAVFH-----HCCSQG 2411 NANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCEEATEVFGMKVDITDHFFNL 2531 SVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHV-IRTVTSGCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALKDV 1898 PEQQLVGIGVMGELVVTGDGLARGYSDKALDENRFVHITVNDQTVKAYRTGDRVRYRIGD 2018 DHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHE 2412 RTLVNFPTDHHLRGSDLLTNRPLQRLQNRRIALEVRERLRSLLPSYMIPSNIVVLDKMPL AVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDI EVINVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVI 1958 GLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVVADH WLGETTRILHDNRSLGNVLEIGTGSGMILFNLD--SRLESYVGLEPSRSAAAFVNKATES FFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRF PGLVEHVEILPKNMEAVNELSAYRYAAVVHVRGSL----LVLPVEKDDWIDFQ 2308 ANQLNQKSLGDLLKSSDAA--IMAVSKIPFEITAFEROVVASLNSNID-----EWQL 1499 1558 1617 1677 1737 12839 1797 1852 2196 2256 13415 2078 13295 2358 13057 13355 13474 g Op δλ ōλ Dβ QY QQ ò g δ QQ Qγ qq δŽ qq δy g Óγ g QQ g Ω Ω Ωy a ΟŊ g qq g q Οy Ω Q ŏ g

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٥y	992	RLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLGIDPATVNV 1044
ДQ	1890	LLPAPPAAHADYEPPSGELERELAHIWQSVLHLDRV 1925
Qy	1045	
Dp	1926	GRHDSFFDLGGHSLLAMQVLGRIESSLGIRTTLRTLFEHPTLHQLADRLSSGAASTTAAA 1985
Oy	1100	IPKSTHEGPVEQSYSQGRLWFLDQLDVGSLWYLIPYAVRMRGPVNVDAL 1148
QQ	1986	
Qy	1149	RRALAALEQRHETLRTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQ 1203
qq	2046	SSALAALVRRHWSLRTVEV-ASPTPAQKICEPEAAPAEVVDLRGTPPDEAEAAARAWASR 2104
Qy	1204	EQTIPFNLSSEAGWRATLLRLGEDDHILTIVWHHIISDGWSIDVLRRDLNQLYSAALKDS 1263
QQ	2105	EQATGFDLARGPVFRARLFRLDHDVCVLVLSTHHIVTDAWSFQPLVRDLAELYRRARGGG 2164
Qy	1264	KDPLSALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSPAKIPTDFARPALLS 1321
Dβ	2165	PADMPELPLQYYDFAVWQRRHLAGKRLADKLAHWTATLRGLPVLELQTDRPRPPVQT 2221
Oy .	1322	GDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRN 1381
Db	2222	FRGAERVLPLDARLVAQLDELARSRGATRFWVLLAALGVLLRRSSGQDDLAIGTAVANRP 2281
٥y	1.382	RPELEDIIGCEVUTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGS 1441
Db	2282	RPELEPLVGFFVNTIVMRLDLGGDPTFEELLSRARVALEAFEHQDAPFEKVVEAVVEAVP-R 2340
	1442	IFAVHSQKDLGRFKFQGLESVPVPSKAYTRFD
Db	2341	RDLSRSPLFQVWLVVQNAPTEALELGEVRIEPLD-LPVEATRFDLRFSVEPRGGRDV 2396
Qy	1498	GSVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVL 1552
Db	2397	ISLQYNVDLFDAATIDRMLATMQSVLSRATQDPAQRVRALSVAPEDRERALVAWNDTAVA 2456
Qγ	1553	NVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPA 1612
QQ	2457	TPDHLRLEEPFFERAVEQPDACAVVDAERRLTYGELARRAEAIAAAASRSGATA 2510
Qy	1613	ETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTA 1672
qq	2511	
Qy	1673	PPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATS 1712
qq	2555	:
. vo	1713	CIPNY
Db	2606	LAYVIYTSGSTGLPKGVMIDHRGAVNTVLDINRRFDVGPEDRVLALSSLSFDLS 2659
٥y	1766	SYEIYSALLFGRTLVCVDYMTTLDARALKDVFFREHVNAASHVTS 1810
Db	2660	
Qy	1811	SSQDVPLRVPRLSRTLMFFFLVVTDSTAPDALDAGGLYQGVQCYNGYGP 1860
qq	2720	ALSSLRLVMMSGDWIPLKLPDRIRAACRAPRVVSLGGA 2757
Οy	1861	TENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLAR 1920
Dp.	2758	TEASIWSIAHPIADVDPAWRSIPYGRPLANQHTYVLDEGLEPCPIGVPGEIHIGGIGVAL 2817
Oy	1921	GY-SDKALDENRFV-HITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIE 1978
Db .	2818	GYWRDEARTRERFLKHPTTGERLYRTGDLGRY-FADGTIELLGRTDHQVKIRGFRIE 2873

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     1336 IALREEYDQQLFDPATIERWAR---HFVLLLESÄVEHPGRPLSELRMLSDAERALLLDDW 1392
                                                                                                                               1393 SGAAAARQAASAPAACVHALFEAHAARQPDATALEFGHORFTYAELSTWSTELALWLRD 1452
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                                                                                   NS----QPLEVQDTLIHHEMLKA-VSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKS
                                                                                                                                                                                       535 LGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVALT
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                                                                                                                                                                                                                                                                  Biotechnologische Forschung mbH
  SAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVV-ADHD 2018
                                 Score 1738; DB 4;
Pred. No. 6.3e-143;
8; Mismatches 857;
                                                                                                                                                                                                                                                       APPLICANT Gesellschaft fuer Biotechnologische For APPLICANT Gesellschaft fuer Biotechnologische For APPLICANT Bristol-Myers Squibb, Co. APPLICANT Beyer, Stefan APPLICANT Bloecker, Helmut APPLICANT Bloecker, Helmut APPLICANT Cino, Paul MAPLICANT Cino, Paul MAPLICANT Goldberg, Steven LAPPLICANT Goldberg, Steven LAPPLICANT Hoffe, Gerhard APPLICANT Mueller, Joachim APPLICANT Reichenbach, Hans TITLE OF INVENTION: Beteropolyketide compounds TITLE OF INVENTION: heteropolyketide compounds GURRENT FILING DATE: 1999-10-07

CURRENT FILING DATE: 1999-10-09

KURBER PERSOLID NUMBER: DE 198 46 493.2

COMPANDE OFFICATION NUMBER: DE 198 46 493.2
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                                                                                                                                                                                 Sequence 93, Application US/09413814. Patent No. 6225064
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27.9%;
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SEQ ID NO 93
LENGTH: 307
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CURRENT APPLICATION DATA:
                 APPLICATION NUMBER: US/08/2
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RREPERBUGE/DOCKET NUMBER: 97
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                       3712 amino acids
                                                                                                                                                                                            NAME/KEY: Modified-site
                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                      amino acid
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                                                                                                                                                    TOPOLOGY:
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                                                                                                                    LENGTH:
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    RDLSRSPLFQVMLVVQNAPTEALELGEVRIEPLD-LPVEA---TRFDLRFSVEPRGGRDV 2389
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Montenegro, Eduardo P.
NENTION: A Method for Influencing Beta-Lactam
WENTION: Antibiotic Production and for Isolation of Large
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COMPUTER: IBM PC COMPATIBLE
OPERATE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Veenstra, Annemarie E. Martin, Juan F. Garcia, Bruno D. Gutierrez, Santiago Barredo, Jose L. Von Doehren, Hans Palissa, Harriet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08222617A Patent No. 5882879
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US-08-222-617A-4
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                                                                                                                                                                                                                                                                                 56 QLDMIDCNALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPALRAFAFTSDSGKTSQ
                                                                                                                                                                                                                                                                                                                                                                                                       206 ESSDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLNDLNASVFPHLSDHLMVPNPTTTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1183 PGIERSVGLFINTLPMIFDHTVCQD----MTALEAIEHVQGQVNAMNSRGNVELGRMSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1344. QTAQLDKWNATAFEYPNTTLHAMFESEAQQKPDKVAVVYEDIRLTYRELNSRANALAFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         533 KSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVA
                                                                                                                                                                                                                                 2 EYLTAVDGRQDLPPTPASFCSH-----GDSPLNSSYEQLFHLYGLDSSRIEAIKPCTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 HRITFP------LSQKALSNSAICRTALSILLSRYTHSDEALFG-AVTEQSLPF
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                                                                                                                                                                         Gaps
                                                                                                                                                               Indels 310;
                                                                                             Length 3712;
                                                                                          atch 9.4%; Score 1516; DB 2; I cal Similarity 26.1%; Pred. No. 4e-123; 564; Conservative 377; Mismatches 912;
/note= "Xaa-Ala or Ser"
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	FEATURE: NAME/KEY: Protein LOCATION: 13665	qa ——	  1695 RVPIGAN
% ; ; %	; OTHER INFORMATION: /label= ACVS ; OTHER INFORMATION: /note= "ACV Synthetase from Acremonium ; OTHER INFORMATION: chrysogenum; aa 1-3665" US-08-222-617A-13	Qy Dp	864 RTGDLAF :     1 1747 KTGDLVF
Que Bes Mat	9.4%; Score 1515; DB 2; Length 3665; 6.1%; Pred. Nol. 4.8e-123; Ve 377; Mismatches 912; Indels 310.	. Oy	920 RSQSANS   1806 RKNDGQK
QY	2 EYLTAVDGRQDLPPTPASFCSHGDSPLNSSYEQLFHLYGLDSSRIEAIKPCTPF 5	QY	980 LPRTATG
Db		qq	
ΟY	56 QLDMIDCNALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPALRAFAFTSDSGKTSQ 115	ογ	
QQ	918AYTMQSMI-HYGVPLKRDIYQAAWQRVQGEHPALR-LRFTWEAEVMQI 963	d d	
δ i	116 VILKDSFVFSWMCWSSSSSPDEVVRDEAAAASGPRCNRFVLLEDMOTKK 165	Oy 4	1088AVVKG
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Vo	166 CQLVWITESHALVDVTFQQRVLSRVFAAYKHEKDTHRPETP 205	· 음	2007 HHDVCLE
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qq		qa	:  : 2127 LDAFYAV
Qy		Qy	1310 IPTDFAR
qa		ପ୍ର	2185 LVPDRPR
Qy	370 GSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRALLLHC 417	QY	1370 DAVIGTP
qq		qa	2245 DITIGIP
Qy	418 QMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEY 472	δÿ	1430 FERVVSA
ΩD	1291 DGDSGCSFTLCYAGELFTDESLQALLDTVRDTLSDILGNIHAPIRNMEYLSSN 1343	qa	2304 FQEITKL
δλ	NWSQPLEVQDTLIHHEMLKAVSHSPTKTALQAWDGDWTYSELDNVSSRLAV	δλ	
qq	1344 QTAQLDKWNATAFEYPNTTLHAMFESEAQQKPDKVAVVYEDIRLTYRELNSRANALAFYL 1403	qa	2357 FDLNVTV
. Oy	533 KSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVA 592	. Qy	1542 GIVTLEKI
qa	1404 LSQAAIQPNKLVGLIMDKSEHMITSILAVWKTGGAYVPIDPRYPDQRIQYILEDTAALAV 1463	qa .	
Oγ	593 LISKLHRETVOKLVGRCVVVDDELLOSVSASDDFSSLTKSQDLAYVIFTSGSTGDPKG 650	Qy	1601 LAGWLRRF
qq	1464 ITDSPHIDRLRSITNNRLPVIQSDFALQLPPSPVHPVSNCKPSDLAYIMYTSGTTGNPKG 1523	qi.	2474 VHLIISS
QY	651 IMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCVCIP 705	οy	1661 GPTIVLIC
QO	1524 VMVEHHGVVNLCVSLCRL-FGLRNTDDEVILSFSNYVFDHFVEQMTDALLNGQTLVVL 1580	qa	2534 ARTLITTE
QY	706 SDDDRMNSIPSFINRYNVNWAMATPSYMGTFSPEDV-PGLATLVLVGEOMSSSVNAIW 762	Οy	1719 TSGSTGRE
qa	1581 NDEMRGDKERLYRYIETNRYTYLSGTPSVISMYEFDRFRDHLRRVDCVGEAFSEPV 1636	đ	-
Οy	763 APKLQSLINGYGQSESSICFASNMSTEPNNMGRAVGAHSWVIDPNDINR 811	Qy	
ΟD	1637 FDKIRETFPGLIINGYGPTEVSITTHKRPYPFPERRTDKSIGCQLDNSTSYVLNDDMK 1694	g .	
. Оу	812 LVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLY 863	Ολ	1834 VTDSTAPD

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GKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLGIDP 1039
                                                                                                                                                                                                                          GKLDAKALPVPDDTVEDD------IVPPRTEVERILAGIWSELLEIPV 1900
                                                                                                                                                                                                                                                               ATFFELGGNSITALKMVNMA-RSVGMDLKVSNIYQHPTLAGIS----- 1087
                                                                                                                                                                                                                                                                                       GD-PLSYTLIPKSTHEGPVEQSYSQGRLWFLDQL----DVGSLWYLIPYAVRM 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVE 1369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKHT-PRGGTVANVPSVVLDSPETLACLNQOSKENPTTSTQKPS--DLAYVIF 2590
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                                                 NRYA - - - - SDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIVVEATK
                                                                                                                      |STSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLE
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964 VDFKSELDWRVVDWTDVSSREKQLVALEQLQTEDLAKVYHLDKGPLMRLYLILLPDSK 1021	166 CQLVWTFSHALVDVTFQQRVLSRVFAAXKHEKDTHRPETP, 205   1022 YSCLFSCHHAILDGWSLPLLFNNVHQAYLDLVEGTASPVEQDATYLLGQQYLQSHR 1077	206 ESSDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLNDLNASVFPHLSDHLMVPNPTTTAE 265	266 HRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFG-AVTEQSLPF 312	313 DKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISŞYDDRLGHLAPFGLRDIRNTGDN 369 1183 PGIERSVGLPINTLPMIFDHTVCQDMTALEAIBHVQGQVNAMNSRGNVELGRMSKN 1238	370 GSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRALLLHC 417   1:1:1   1:1	418 QMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEY 472	473 DRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTALQAWDGDWTYSELDNVSSRLAVHI 532   1::	533 KSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLLIDPNDPPARTAQVVTQTRATVA 592 1404 LSQAAIQPNKLVGLIMDKSEHMITSILAVWKTGGAYVPIDPRYPDQRIQYILEDTAALAV 1463	593 LTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQDLAYVIFTSGSTGDPKG 650 :	651 IMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCVCIP 705 :1:1	706 SDDDRMNSIPSFINRYNVNWMMATPSYMGTFSPEDV-PGLATLVLVGEOMSSSVNAIW 762 :   :	763 APKLQLLNGYGQSESSICFASNMSTEPNNMGRAVGAHSWVIDPNDINR 811	812 LVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLY 863	864	920 RSGSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLE 979   1	980 LPRTATGKIDRRKLRIMGKDILDKQTQGAIVQQARADIPVFADTAAKLHSIWVQSLGIDP 1039 1	1040 ATVNVGATFFELGGNSITAIKMVNMA-RSVGMDLKVSNIYOHPTLAGIS 1087 ::::            : ::       :  :   :  :	1088AVVKGD-PLSYTLIPKSTHEGPVEGSYSOGRLWFLDQLDVGSLWYLIPYAVRM 1139
QQ	QY Db	Qy Db	QY Db	Qy	Qy Db	QY	Qy Db	Qy Db	Qy	Qy	Qy	Qy	Qy	Qy Db	Qy	Qy	Qy	Qy Dp
Db 2704 GEBFHASQFEKMRSQFAG-QINNAYGITETTVYNIITTFKGDAPFTKALCHGIP 2756	QY 1890 NSGAYVVDPEQQLVGIGVWGELVVTGDGLARGY-SDKALDENREVHITVNDQT 1941	QY 1942 VKAYRTGDRVKYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQ 2001 :	Qy 2002 NED 2004 :   Db 2876 DED 2878		AP 882 ORM :	<pre>: Martin, Juan : Garcia, Brunc : Gutierrez, Sa : Barredo, Jose</pre>	hren, Hans , Harriet mpt, Henk gro, Eduardo P.	; TITLE OF INVENTION: A Method for Influencing Beta-Lactam; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large; TITLE OF INVENTION: Quantities of ACV Synthetase; NUMBER OF SOURCES: 27	CORRESTONDENCE ADDRESS: ADDRESSE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive CTTY: Chicago	34 15	## MELUM TYEE: KIOPPY 418K COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPACTION COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS SYSTEM: PATENTIN Release #1.0, Version #1.25	CURRENT AFFLICATION DATA:  APPLICATION NUMBER: US/08/222,617A  FILING DATE: 04-APR-1994  CLASSIFICATION: 435	ATTORNEY ACENT INFORMATION:   REFERENCE/DOOKET NUMBER: 97,157 	= ± ∴ ≥ ∶	Ouery Match  Query Match  Query Match  Best Local Similarity 26.18; Pred No. 4.9e-123;  Matches 564: Conservative 377: Mismatches 912: Indels 310: Gans 80:	2 EYLTAVDGRQDLPPTPASFCSHGDSPLNSSYEQLFHLYGLDSSRIEAIKPCTPF 5   1   1   1   1   1   1   1   1   1	50 QLDMIDCNALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPALRAFTSDSGKTSQ	116 VILKDSFVFSWMCWSSSSSPDEVVRDEAAAASGPRCNRFVLLEDMQTKK

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                                                                                          IPTDFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVE 1369
                                                                                                                                                              DAVIGTPIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIP 1429
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                                       LDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHIL---TIVMHHIISDGWSIDVLRRD
                                                      LVPDRPRPAQFDYTGNDLQFSTTPETTAQLKELAKREGSSLYTVVAAAYFLLLYVYTNQR
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

Sequence 3464, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:

US-09-134-001C-3464

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTVHTLVKLINGIYMQITQNPSLL--IKDIKLSDRSDLAKINDINLQNNDINYSEVTYKT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTHLN---DLNASVFPHLSDHLMVPNP-----TTTAEHRITFPLSQKALSNSAIC 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSICFASNMSTEPNNMGRAV-----GAHSWVIDPNDINRLVPIGAVGELVIESPGIAR 830
                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVALTSKLHRETVQKLVGRCVV 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATPSYMGTFSPEDVPGLATL--VLVGEQMSSSVNAIWAPKL-----QLLNGYGQSES 777
                                                                                                                                                                                                                                                                                                                                                                                                      --TYQTVAPLRVHCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 VWIVSIYLAHHFISQSSDVTLGI------HFSIDNKNTENMMYLNTDIAPLLSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : | : : : | : | : | | 441 VVERFERQVHQHPDSIALQYEQRSMTYHQLNQCANLLAYRLRLNHQIEPNDMVALIAERS
                                                                                                                                                                                                                                                                                                                                                                             68 QSAIGHAV---YDVPTDIDISRFALAWKEIVNQTPALRAFAFTSDSGKTSQVILKDSFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 SWMCWSSSSSPDEVVRDEAAAASGPRCNRFVLLEDM--QTKKCQLVWTFSHALVDVTFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRVLSRVFAAYKHEK-----DTHRPETPESSDATDTDSQSVSVVSMSCEDNAVSATHFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLPLFN-FKIYQFLDEAYLLLDFHATIFNESQLTPFLQQLNIAYTHSLKSEYSISDFYNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNLRASDVMDAISSYDDRLGHLAPFGLRDIRNTGDN----GSAACDFQTVLLVTDGSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L----KAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                    Length 2404;
                                                                                                                                                                                                                                                                                                                                            431;
                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTALSILLSRY--THSDEALFGAVTEQSLPFDKHYLADG----
                                                                                                                                                                                                                                                                                              8.8%; Score 1425.5; DB 4;
23.2%; Pred. No. 1.7e-115;
Live 466; Mismatches 1032;
              FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                              ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3464
                                                                                                                                                                                                                                                                                                                                          Conservative 466;
                                                                                                                                                       NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3464
LENGTH: 2404
                                                                                                                                                                                                                                                                                                                   al Similarity
582; Conserva
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM:
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Best Local S
Matches 582
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qq	730 TTFTTTFAI-PQEMPSRIPIGLPISGTTVYVMQGDRICGVGVPGELCIGGAGLAK 783	6
Qy	831 DYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLYRTGDLARYASDGSIVCLGRIDS 885	1883
qq	:	Db 1764 PIGKPLANVDIFIMS-GG
Qy	886 QVKIRGQRVELGALETHLRQQMPDDLTIVVEATKRSOSANSTSLIAFLIGSSYFGNRPSD 945	Qy 1942 VKAYRTGDRVRYRIGDGL
qa		Db 1822 -QLYRSGDLARL-MPDGQ
0y	946 AHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQT 1005	Qy 2002 NEDQAPEILGFVVADHDH
qq		1880
Qy	1006 QGAIVQQAPAPIPVFADTAAKEHSIWVQSLGIDPATVNVGATFFELGGNSITAIKMVN-M 1064	QY 2062 TSMYDGSQIDFDEMHEWL
අු	: : :	Db 1930KVDESRLPVPNVHKNK
ò	1065 ARSVGMDLKVSNIYOHPTIAGISAVVKGDPLSVTLIPKSTHEGEVFOSVSOGRIMET 1121	Qy 2119 LEPSRSAAAFVNKATESI
5 음	979 EERLKKRLKVGDLMKSPTVEQLGQQIEELQNDVYEVIPKANESYQYDLSASQKSMYLL 1036	Db 1975DFFEMGGTSI
ò	1122 DOLDVIGSTAWLIEVAVRARCEVINDALERALEAREROPHETTERFORMANDICVICTORIES	Qy 2179 LAEIADTLI
3 6	1027 UNIVERSE PROPRIET TO SEE THE SECOND SEC	Db 2014 IANHTEKRQALPEVVLPD
3 6	MININENDIY TULFE DRAKESSELINVRIQUENTALIBERTETURIQIY Y DUDNEVRUKTALIHV	Qy 2224K
÷ 1	ILOZ SEBMNYIDLOGSUDUPFEVENDEGITYFNUSSEAGMNATLIKUGEDUHLUTIVMHHILISD 1241	Db 2072 LIDEMQDDADQITCIVRG
qq	1097 SPDFEEVTTSLTNEQDIIQSFMEPFDLEQPSQMRVKYIHGPQQDY-LFMDTHHSIND 1152	Ov 2267 KNMEAUNEI SAYRYA
Qy	1242 GWSIDVLRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQ 1301	
qq	1153 GMSNTILLSDLNALYQDKSLPELKLQYKDYSEWNVHRDLSKQRHFWLQQ 1201	
Qy	1302 LKDSSP-AKIPTDFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRA 1360	Qy 2324 DAAIMAVSKIPFEITAFE   :: :
qq	1202 FENOVPILNMPTDYPRPSIKTTNGNNLTFHYNROIKGOLKSSYVEGHOVTDFMFPASAINV 1261	Db 2176 KAKLIYISTI
à	AHVRI TAVEDANI CTDIANDANDERI PRI I CCEVANO CADINI DU UN DELL'ARTHUR	Qy 2384 FRVEVSSARQWSQNGALE
Ž i	::   :         :  :   :   :	Db 2211 FTSPYTKSKFYSEIKVLE
gg	1262 LLHKYTRQDDIAIGSVISARTHRDTENMLGMFANTLVYRGRPHDQKTWDQLMAEMKEMCL 1321	
ΟŊ	1421 AAFENEDIPFERVYSALQPGSRDLSSTPLAQLIFAV-HSQKDLGRFKFQGLESVPVPSKA 1479	RESULT 8
QQ	1322 GAYEHQEYPFESLVNDL-VDERDASHNPLFDVMLVLQNNETNHANFGHSQLTHIP-PQST 1379	Sequence 11, Application US/09
Qy	1480 YTREDMEFHLEQETDSLKGSVNFADELFKMETVENVRVFFEILRNGLQSSRIPVSILPL 1539	; Patent No. 6225064 ; GENERAL INFORMATION:
QQ	1380 TAKFDLSFIIEEDQDDYVVNIEYNTDLYKQETIHHIAEQLQMIIKHVISTENLKIQDIDE 1439	<pre>; APPLICANT: Gesellschaft fuer ; APPLICANT: Bristol-Myers Squi</pre>
ΔO	TI EKI DVI NVKHVDYDBESSI ADVIDATAVA V DRGI ADVIDATA V DR	
[3 d		, APPLICANT: BIOCKET, REIMUL; APPLICANT: Brandt, Petra
ga	1440 NDDLLIWLDKHVNDCSLDLPKNKSIQQLLHDVMKAKADDVALKMNGQSMTYQEL 1493	Cino, Pau Dougherty
οy	1595 DRQSDILAGWLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQD 1654	, APPLICANT: Goldberg, Steven I
qq	1494 DDYSNSMAQTLIQNGIQKGERVALLTERSFEMVASMIAVLKVGGSYVPIDVTYPDKRIEF 1553	, APPLICANT: Mueller, Joachim
٥y	1655 ILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPS 1709	; AFFLICANT: Kelchenbach, Hans ; TITLE OF INVENTION: DNA seque
qq	:	<pre>; TITLE OF INVENTION: heteropol ; FILE REFERENCE: PCT/US 99/235</pre>
òO	1710 ATSTAVULYTSGSTGRPKGVWIEHRVITRTVTSGCTDNVPSETBWAHMATTAFDGA 1765	; CURRENT APPLICATION NUMBER: U
7 සි	MYHIYTSGTTGKPKAVSVKORNIINLVCAMTKRLNLSDDEVYLOYANVYFDAS	EARLIER FILING DATE: 1998-10-
ò	COVETVCALI ECEMITAVAVAVAMENT DA DAT VOLUMA A CUIVA A CUIVA COCCADATA VA COLORA DA COLO	NUMBER OF SEQ ID NOS: 107
<b>3</b> 8	ATDEYCSLINGYPLYIATSVERTUNTDLEKLISOENTITAS	; SOFIWARE: FALENCIN VET. 2.1 ; SEQ ID NO 11 : LENGTH: 2628
ë	2	; TYPE: PRT
δ 1		; OKGANISM: Soranglum Cellulos US-09-413-814-11
<b>අ</b> .	1704 VMHHFYIPKVITGGAPSTPAFVQHISKHCDMYVNAYGPSENTVITSCWIYEKGDAIPSTI 1763	

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YAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLKSS 2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIPSLAGKAKVQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEY 2178
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SLDAMVVVSKL-----KSNGIH---ITMQDVXQ-FKTVRY 2013
                                                                                                                                                                                                                                                                                                                 --HLPNVQRIFFGDVRSQATNEHFLAARAIHTLGKNAT----- 2223
                                                                                                                                                                                                                                                                                                                                                                                                 QQLVGIGVMGELVVTGDGLARGYSDK-ALDENRFVHITVNDQT 1941
                                                                                                                          DHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGW 2061
                                                                                                                                            ILGETTRTLHDNRSLGNVLEIGTGSGMI---LFNLDSRLESYVG 2118
                                                                                                                                                                                                              ||| :| : : | | ::| BDHLPQLQSLV--ERRYQLKSQHLTQSSLGHVLLTGATGFLGAY 2071
                                                                                                                                                                                                                                                                                                                                                                               KDDVROKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILP 2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAG 2383
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80; 1171 83	1224	1284	1341	1401	1457	377	431	1574	1634	1691	610	1,4,	1804	7859	692	1919	826	1977	2037	931	2097	971
62; Conservative 341; Mismatches 843; Indels 474; Gaps SYSOGRLWFLDQLDVGSLWYLIPYAVRMGPVNVDALRRALAALEQRHETLRTTFEDDDG 1:1	VGVOIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLSSEAGWRATLLRL 	GEDDHILTIVWHHIISDGWSIDVLRRDLNOLYSAALKDSKDPLSALTPLPIQYSDFAKWQ 	KDOFIEQEKQLNYWKKQLKDS-SPAKIPTDFARPALLSGDAGCVHVTIDGELYQSLRA ::	FCNEHNITSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDIIGCFVNTQCMRIN :			DAT	VVRVFFEILRNGLQSSRTPVSILPLIDGIVTLEKLDVLNVKHVDYPRESSLADVFQTQVS :	AYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAVFAPRSCETIVAFFGVL    :	KANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALN	NAGGATVPLDFITYPSEKL-GLMMADAAPSVLLIQASLLSKLPPHGDATLVQLDALHEALS DSNADGFEVIEHDSTKPSATSTAVVLVTGGGGGDAKGWATFUDVTFPWVMGGGTDN	RLPHHTPRSGVTAQNLAYVMYTSGSTGRPKGVLVEHRGLCNLPTVQAKLYGI	YPSETRWAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALKDVFFREHVNA	ASHVISSSODVELKVPRRISRILMFFFLVVTDSTAPDALDAGGIVGGVGVVGV	. >	ALNNSGAYV	PIETTIWASSAADLSDERIPPIGRPIANTQIYVLDEALEPVPIGVPGEIFIGGVGVA	RGYSDKA-LDENRFVHITVND-QTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRI     :	ESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVVADHDHSENDKGQSANQVEGWODH		ESGMYSDIGEIDPSTIGSDFKGWT : : :    :	AELRQSVSERLPATMVPSSFVALDALPLTPNGKVDRRALP
111	1172	1225	1285	1342	1402	1458	378	1515	1575	1635	ი თ	-	1748	1805	722	1860	770	1920	1978	886	3	932
Matches Qy Db	oy Ob	Oy Db	Qy Db	O.Y Db	oy 1	3 6	. q	Qy Db	Qy Db	. 40 40	2 6	g q	yo 4	λo	Ob	٥y	qq	Qy Dp	Οy	qq	Qy.	qq

qa	972	:	7
δy	2158	DLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVR 220	01
Dp	982	:     : :     : :     HAPPRINAVEEELARIWASVLRLERVGVHDNFFEIGGDSILSIQIVVRAQQAGLRLTPRQM 104:	41
Oy	2202	GKNATKDDV	43
QQ	1042	FQHQTIABLSTVARAVEAVHVEQDPVTGPAPLTPVQRWWLEQEAAEPHHFNQSIFLEV 1099	66
δ, i	2244	DELVLPV 229	6
DD	0	STPFQRVDLGALP- 115	
yo 4	6 1	KDDWIDFQANQLNQKSLGDLLKSSD-AAIMAVSKIPFEITAFERQVVASLNSNID 2	53
QC	1126	SAEQISAMEKAASEAQASLDLAAGPVVRAVLFDLGEVAPQRLLVIAHHIAVD 1207	02
Οy	2354	LD 24	01
Ob	1208	ILLDDLFGAYEQARRGEAVRLPPKTTSVKRWAELLTEHAGSE 125	54
Qy	0	QGRILVNEPTDHHLRGSDLLTNRPLORLONRRIAIEVRERLRS 245	52
qq	1255	AVKAELGYWLDSSRRTVAPLPVDRR-AGEDVWGSARHIVVSLTPEQTEQLLREVPQAYRT 1313	13
Qy	2453	247	77
qq	1314	LDLEGHGREELAGVDLTRTVGWFTAMYPILLRV 137	20
Οy	2478	EEATEVFGMKV 252	22
qa	1371	:	19
Qy	2523	LGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIRQGLGLQQPVS 258	82
qa	1420		40
Qy	2583	SQGQDRSAHMAPRTETEAILCDEFAKVLGFQVGITDNFFDLGGHSLMATKLAVRIGH 264	0 \$
QQ	1441	PGAHRAHLIEVNASIANGRLYATWIYSERRH 147	6.
Qy	2641	OSKTNEIVGGREMAEYSPFOLLFTEDPEEFMA 27	00
οgα	1480	EPETIERVAASFVTALRALIAHCTLPEVGGNTPSDFDKVRLR-QETIDALDA 1530	30
δý	2701	HTTARPRPEVPEYIDEPSTSEPDAAGLI 275	57
Db	1531	: :	88
٥y	2758	CESLVNHLDIFRTVFAEASGELYQVVLSCLDLPIQVIETEDNINTATNEF 280	60
Db	1589		38
Qy	2810	LDEFAKEPVRLGHPLIRFTIIKQTK-SMRVIMRISHALYDGLSLEHVVRKLH 2860	20
Db	1639	TAHISRYVEAERQERFDLRKAPLARAGLELRLRKDAWCLVETIHHLILDGWSTQILLKEVF 1698	86
Οy	2861	MLYNGRTPMT 2902	02
QQ	1699	TLYEAHRGHRGHLALELEQPRPYGDYIGWLAKQDQVRTAAFWRRELEGFSAPTPLGVDRA 1758	89
Qy	2903	LSDDTVVDGNDATCKALHLSKIVNIPSQVLRGSSNIITQATVFNAACALV 295	33
qq	1759	VPHDDGGPREGWRRIALSGDDAARLAAFARQHQLTMSTLVQGAWALL 1805	2
Qy	2954	LSRESDSKDVVFGRIVSGRQGLPVEYQDIVGPCTNAVPVRAHIESSDYNQLLHDIQDQ 3011	-
qq	1806	LSRYSGDPDVLFGMTVSGRSAPIPGIERMTGLFINTIPVRVR-EPADASVLAWLKALOEH 1864	4
0y	3012	YLLSLPHETIGESDLKRNCTDWPEAITNESCCITYHNFPYHPESGFEQQRVEMG 3065	5

1962   PARTICHERISPICATIONAL SUVPRESTRINGENERPOLITIES   1916   1906	362 RYLRSIGILPEQ-LVALFLDKSEKLIVTILGVWKSGAAYVPIDPTYPDERVRFVLDDTKA 4	590 TVALTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQDLAY 6 1	638 VIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLE- 6	692IMTTLINGGCVCIPSDDDRMNSIPSFINRYNVNMMATPSYMGTFSPEDVPGLA 7	746 TLVLVGEQMSSSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRAV-G 7 ::     ::     ; ;        ; ;	799 AHSWVIDPNDINRLVPIGAVGELVIESPGIARDXIVPPPPEKSPFFTDIPSWYPA 8 :::: : :	854 NTFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTI 9 	914 VVEATKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIP 9	972 SFYICMLELPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIW 1 : : : :	1032 VQSLGIDPATVNVGATFFELGGNSITAIKMVNMARSVGMDLKVSNIYQHPTLAGISA 1	1089 VVKGDPLSYTLIPRSTHEGPVEGSYSGGRLWFLDQLDVGSLWYLIP 1 ::	1135. YAVRMRGPVNVDALRRALAALEQRHETLRTTFEDQDGGVGV 1 :   :   :	1175 QIVHEKLSEEMKVIDLCGSDLDPFEVLNOEOTTPFNLSSEAGWRATLLRLGEDDHILTIV 1	1235 MHHIISDGWSIDVLRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQ 1	1295 LNYWKKQLKDSSPAKIPTDFARPALLSGDAGCVHUTIDGELY-QS 1	1339 LRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDIIGCFVNTQ 1 	1397 CMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERV-VSALQPGSRDLSST 1 : : :     :	1448 PLAQLIFAVHSOKDLGREKEOGLESVPVPSKAYTREDMEFHLEQETDSLKGSVNFAD I	1505 ELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHVDYPRESS 1 
1865 EARLICHRISPLUSDANH-SDVPRGTPLERSLVVPRN-TFVQVIFEAPPWEEPTREES  3066 VLINKWANIE-MORPLUDALAGEVEPDGGGLAVVAYATGUCERRKEBLOGAVERSLITILE  1921 LRHIDAGYISDPPYPLTALAGEVEPDGGGLAVYATAGTUCERRKEBLOGAVERSLITILE  1922 LRHIDAGYISDPPYPLTALAGEVEPDGGGLAVYATAGTUCERRKEBLOGAVERSLITILE  1923 LRHIDAGYISDPPYPLTALAGEVEPDGGGLAVYATAGTUCERRKEBLOGAVERSLITILE  1924 CRHIDAGYISDPPYPLTALAGEVEPDGGGLAVYATAGTUCERRKEBLOGAVERSLITILE  1925 CRHIDAGYISDPPYPLTALAGEVERSLITICATICATICATICATICATICATICATICATICATIC	qa	Qy Dp	QY.	Qy Db	Qy	Qy	Qy	do ·	Qy Db	Qy	Qy Dp	Qy	Qy	Qy Db	oy Db	Qy Db	Qy	Qy	Qy
1865 EARLICHRISPLUSDANH-SDVPRGTPLESSLVVPBN-TPVQVIFEAPPWEEPTREES  3066 VLANKWANIE-MORPLYDALAGEVPEPDGGGLAVVAYATGVFERARFDDGAVERHYEPETREES  1921 LRHIDAGYISDPPYPLTALAGEVPEPDGGGLAVYATAGTGFRRREDDGAVERHIGHTTLAGE  1922 LRHIDAGYISDPPYPLTALAGEVPEPDGGGLAVYATAGTGFRREDDGAVERHIGHTTLAGE  1923 LRHIDAGYISDPPYPLTALAGEVPEPDGGGLAVYATAGTGFRREDDGAVERHIGHTTLAGE  1924 CRHIDAGYISDPPYPLAGATT  1925 GATCLAGATT  APPLICANT  AT												<del></del>						<u> </u>	<del></del>
	1865 EAELLEHEHSPLVEVQAH-SDVPRGTPLFESLVVFENYPVQVIFEAPPVEGPTRAEEG	3066 VLTKEVNIE-MDEPLYDLAIAGEVEPDGACLKVTVIAKTQLFGRKRVEHLLEEVSKTFEG 	ESULT 9 S-08-222-617A-27 S-08-222-617A-27	Dequence 2/, Approaction 05/06/2201/A Patent No. 5882879 GENERAL INFORMATION: APPLICANT: Veenstra, Annemarie E.	Martin, Jue Garcia, Bru Gutierrez, Barredo, Jo	. 5	OF INVENTION: A MECHOD IN INITIATION OF INVENTION: Antibiotic Production and for Isolation of OF INVENTION: Quantities of ACV Synthetase  OF SEQUENCES: 27	Boehnen Hulbert cker Drive	COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM:	disk patible -DOS/MS-DOS elease #1.0, Version	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/222,617A FILING DATE: 04 APR-1994 CLASSIFICATION: 435	: 97 27:	TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein 5-08-222-6174-27	8.3%; Score 1342.5; DB 2; Length 3727; 21.2%; Pred. No. 9e-108; vative 515; Mismatches 1232; Indels 963; Gaps	312 FDKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISSYDDRLGHLAPFGLRDI	364RNTGDNGSAACDFQTVLLVTDGSHVNGINGFLQOITESSHF-MPCNNRALLHCQM	420 ESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMT	471 EYDRAEIESWNSQPLEVQDT-LIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLA 302 APOKOOI FFWANNDGFVESKPIHHITFFYVPDHFNATAVORDEPTWYGFVANOORGI	530 VHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRA ::: : : : : : :  :: : : : : : : : : : :

RESULT 10 US-08-222-617A-2 : Sequence 2, Application US/08222617A : Patent No. 5882879	RE US	2229 QKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELSAY 2278 :	Qy Db
2976 PVEYQDIVGPCTAAVPVRAH 2999 ::::         :   :   3356 ALQHIAPTGPSMVTIEGH 3377	da ———	2190PNYQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVR 2228   1   1   1   1   1   1   1   1   1   1	Qy Dp
CKALHLSKIVNIPSQVLRGS:     : ::   :   GSRVRLSRSLS-PEKT	qa —	2158DLHPDLVVLNSVIQYFPSSEVLAEIADTLIHL 2189 	Oy Dp
	<b>q</b> 0	2142 VQFKYDGDDLSIELSKKETENLRGVARRCKSSLYVVLVSVYCVMLASYANQSDVSVGIPV 2301	S S
2862	- KO	RMRNLSDFWLRKLIGLEPLQLITDRPRP	ପ୍ର ଓ
2806 TNEFLDEFAKEPVRLGHPLI: 	O O		oy.
3146 TPELDVDSLSAAVRDLQQYHDVFR	qa	2112	Oy Db
3108	අ <sub>ධ</sub> :	:   :	QΩ
	δō	LFNLDS	٥y
2028 SEMATKLAVKIGHKEDTTYSVKDV  ::  :: : :: :: : : 3058 SITSLHLVAQIHNQVGCKITVRDI		2045DIGEIDPSTIGS	Oy Op
		2034 WQDHFESGMYS	oy do
2944	qa ———	REMOSRLPGYMVPSRLILVSKFPVTPSGKLDTKALPPAEEESEIDVVPPRSEIERSLCDI	- qa
2527	٥٧	1827 DFQVKIRGLRIEVGEIEALLSSYHGIKQSYVIAKDCREGAQKFLVGYYVADAALPSAAIR 1886	a ò
2518 F	λο -	1967 DTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEIL-GFVVAD 2016	QY
2464 :VVLDKMPLNANGKVDRKELSRRAK   :  :    2830 -ALQPVPFDANGELYLAGD	. Oy	1916 DGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDRVRYRIG-DGLIEFFGRM 1966 11	Qy Db
	ලි අධ 	1858 YGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTG 1915	Qy Db
2712 VLSGH	qa :		qa
2408 CSQGRTLVNFPTD	δ	RE-HVNAASHVISSSQDVPLRVPRRLSRILMFFFLVVTDSIAPDALDAOGLXOGVOCYNG	δ
2387 EVSSARQWSQNGAL	λδ — —	1744 CIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCV-DYMTTLDARALKDVFF 1798 :	Qy Db
2339AFERQVASLNSNIDEWQ 1 : 1   : 1 : 1 : 1 : 2594 LEEIKAKAVLVHSSHASKCERHGA	ž da	1684 VRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTSG 1743 : : : :     :     :	Qy Db
2534	<b>q</b> a 		qa
2307 QANQLNQKSLGD	λο 		Οy
: :   2474 RPTENGDLHLPLAQSPLATTAEEQ	q <sub>Q</sub>	1419 LHEMFENEASCRPDKIAVYEETSLTYRELNERANRMAHQLRSDVSPNPNEVIAVMERS 1478	7 A
2279 RYAAVVHV	^o		Ċ

Qy	2279	
QQ	2474	:  :   : : RPTENGDLHLPLAQSPLATTAEEQKVASLNQAFEREAFLAAEKIAVVQGDRALSYADLNG 2533
δ	2307	QANQL NQKSLGD 2338
qq	2534	QANQLARYIQSVSCIGADDGIALMLEKSIDTIICILAIWKAGAAYVPLDPTYPPGRVQLI 2593
QY	2339	AFERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRV 2386
ΟP	2594	LEEIKAKAVLVHSSHASKCERHGAKVIAVDSPAIETAVSQQSAADLPTIASLGNLAYI 2651
QY	2387	1
qq	2652	LLRD
Qy	2408	-
QQ	2712	VLSGHKLIVPPAEFVADDEFYRMASTHGLSYLSGTPSLLQKIDLARLDHLQVVTAAGEEL 2771
QY	2445	
Db	2772	HATQYEKMRRRFNGPIYNAYGVTETTVYNIIAEFTTNSIFENALREVLPGTRAYVLTA 2829
Oy	2464	,
QQ	2830	DQRFIPN
Qy	2518	E
qq	2884	YKTGDLVRSRFNRQQQPQLEYLGRGDLQIKMRGYRIEISEVQNVLTSSPGVREGAVVAKY 2943
Qy	2527	HFPNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLA 2568
qq	2944	ENNDTYSRTAHSLVGYYTTDNETVSEADILTFWKARLPTYMVPSHLCCLEGALPVTINGK 3003
Qy	2569	SVIRGGLGLQQPVSDGQGQDRSAHMAPRTETEAILCDEFAKVLGFQ-VGITDNFFDLGGH 2627
qq	3004	LDVRRLPEIINDSAQSSYSPPRNIIEAKMCRLWESALGMERCGIDDDLFKLGGD 3057
Qy	2628	SLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAEYSPF 2687
QQ	3058	SITSLHLVAQIHNQVGCKITVRDIFEHRTARALHDHVFMKDSDRSNVTQF 3107
QY	2688	QLLFTEDPEEFWASEIKPQLELQEIIQDIYPSTQMQKAFLFDHTTARPRPFVPFYIDFPS 2747
Db	3108	RTEQGPVIGEAPLLPIQDWFLSKALQHPMYWNHT4FYVR 3145
QY	2748	TSEPDAAGLIKACESLVNHLDIFR-TVFAEASGELYQVVLSCLDLPIQVIETED-NINTA 2805
qq	3146	TPELDVDSLSAAVRDLQQYHDVFRMRLKREEVGFVQSFAEDFSPAQLRVLNVKDVDGSAA 3205
Οy	2806	TNEFLDEFAKEPVRLGHPLIRFTIIKQTKSMRVIMRISHALYDGLSLEHVVRKLHM 2861
Db	3206	VNEILDGWQSGFNLENGPIGSIGYLHGYEDRSARVWFSVHHMAIDTVSWQILVRDLQT 3263
Qy	2862	LYNGRSLLPPHQFSRYMQ-YTADGRESGHGFWRDVIQNTPWTILSDDTVVDGNDAT 2916
Db	3264	LYRNGSLGSKGSSFRQWAEAIQNYKASDSERNHWNKLVMETASSISALPTST 3315
Q.	2917	CKALHLSKIVNIPSQVLRGSSNIITQATVFNAACALVLSRESDSKDV-VFGRIVSGRQGL 2975
рþ	3316	GSRVRLSRSLS-PEKTASLIQGGIDRQDVSVYDSLLTS-VGL 3355
Qy	2976	PVEYQDIVGPCTNAVPVRAH 2995
Db	3356	ALQHIAPTGPSMVTIEGH 3373
RESULT US-08-2 ; Seque ; Paten	10 122-617A ince 2, it No. 5	ULT 10 08-222-617A-2 equence 2, Application US/08222617A atent No. 5882879

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                                              TLVLVGEQMSSSVNAIWAP--KLQLLNGYGQSESSSI----CFASNMSTEPNNMGRAV-G
                                                                               RIILVGENLTEARYLALRORFKNRILNEYGFTESAFVTALKIFDPESTRKDTSLGRPVRN
                                                                                                                AHSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPP--PPEK---SPFFTDIPSWYPA
                                                                                                                                   VKCYILNPS--LKRVPIGATGELHIGGLGISKGYLNRPELTPHRFIPNPFQTDCEKQLGI
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APPLICANT: Garcia, Bruno D.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutlerrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Von Doehren, Hans
APPLICANT: Von Doehren, Hans
APPLICANT: Von Liempt, Hens
APPLICANT: Wontenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYDRAEIESWNSQPLEVQDT-LIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVALTSKLHRETVQKLV----GRCVVVDDELLQSVSASD------DFSSLTKSQDLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 VTYTSGTTGFPKGIFKQHTNVVNSITDLSARYGV-----AGQHHEAILLFSACVFEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | : | | : | EAARGSEKESVTAID-----SASSLVKMGLFDLLVSFVDADDARIPCFDFPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTH-----AFGACLLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 FDKHYL----ADGTYQTVAPLRVHCQSNLRASD----VMDAISSYDDRLGHLAPFGLRDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                    SSEE: McDonnell Boehnen Hulbert & Berghoff
F: 300 South Wacker Drive
Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 9.3e-108;
; Mismatches 1232;
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21.2%; Pred. No. 9.3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3778 amino acids
TYPE: amino acid
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                 Annemarie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                 Veenstra,
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-222-617A-2
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY
                                                                                                                                                                                                                                                              STREET:
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Matches
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us-09-482-788-2.rai

		1	EVSSARQWSQNGAL-
qq	1597 SKVFGLRDTDDEVILS-FSNYVFDHFVEQMTDAILNGQTLLVLNDGMRGDKERLY 1650	7652	IFTSGTSGKPKGVLV
δλ	1799 RE-HVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDAGGLYQGVQCYNG 1857	2408	CSQGRILVNFPTD-
qq	1651 RYIEKNRVTYLSGTPSVVSNYEFSRFKDHLRRVDCVGEAFSEPVFDKIRETFHGL-VING 1709	2712	VLSGHKLIVPPAEFV
δλ	1858 YGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTG 1915	Oy 2445	EVRER
q	1710 YGPTEVSITTHKRLYPFPERRMDKSIGQOVHNSTSYVLNEDMKRTPIGAVGELYLGG 1766	7/17	I EKMKKE'N
ΟŸ	1916 DGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDRVRYRIG-DGLIEFFGRM 1966	2464	VVLDKMPLNANGKVDI
qa	1767 EGVVRGYHNRADVTAERFIPNPFQSEEDKREGRNSRLYKTGDLVRMIPGSSGEVEYLGRN 1826.	2830	-ALQPVPFDAVG
οy	1967 DTGFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEIL-GFVVAD 2016	2518	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Dp	1827 DFQVKIRGLRIEVGEIEALLSSYHGIKQSVVIAKDCREGAQKFLVGYVVDAALPSAAIR 1886	2884	YKTGDLVRSRFNRQQ(
Qy	2017 2033	2527 -	HFFNLGGHSLLA
<b>Q</b> Q	1887 RFMGSRLPGYMVPSRLILVSKFPVTPSGKLDTKALPPAEEESEIDVVPPRSEIERSLCDI 1946	2944	ENNDTYSRTAHSLVG
Qy	2034 WQDHFESGMYS 2044	Qy 2569 SVIRQGEGLQQPVSDC	SVIRQGLGLQQPVSDC : :   :::
Dβ	1947 WAELLEMHPEEIGIYSDFFSLGGDSLKSTKLSFMIHESFNRAVSVSALFCHRTVEAQTHL 2006		בום בייב
ΟŊ	2045DIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGE 2081	2628	SLMATKLAVRIGHRLI
Op	2007 ILNDAADVHEITPIDCNDTQMIPVSRAQERLLFIHEFENGSNAYNIDAAFELPGS 2061	3058	SITSLHLVAQIHNOVO
οy	2082 TTRTLHDNRSLGN 2111	2688	QLLFTEDPEEFMASE
Db	2062 VDASLLEQALRGNLARHEALRTLLVKDHATGIYLQKVLSPDEAQGMFSVNVDTAKQVERL 2121	3108	TEQGPVIGE
δy	2112	2748	TSEPDAAGLIKACESI
QQ	2122 DQEIASLSQHVFRLDDELPWEARILKLESGGLYLILAFHHTCFDAWSLKVFEQELRALYA 2181	3146	TPELDVDSLSAAVRDI
Qy	2118 GLEPSRSAA 2126	2806	TNEFLDEFAKE
qq	: ::    2182 ALQKTKSAANLPALKAQYKEYALYHRRQLSGDRMRNLSDFWLRKLIGLEPLQLITDRPRP 2241	3206	LDGWQSGFN
٥y	2127AFVNKATESIPSLAGKAKVQVGTATDIGQVD 2157	Qy 2862 LYNGR	LYNGRSLLPPHC
. q		3264	LYRNGSLGSKGSSFR
δλ	2158DLHPDLVVLNSVIQYFPSSEYLAEIADTLIHL 2189	2917	CKALHLSKIVNIPSOV :   : ::   :
qq			GSRVRLSRSLS-PEK1
Qy	2190ATKDDVR 2228	2976	PVEYQDIVGPCTNAVE
qq	2359 LLQVDNDPSRHPLVQNVFNFESRANGEHDARSEDEGSLAFNQYRPVQPVDSVAKFDLN 2416	Db 3356 ALQHIAPTGPSMV7	IAPTGPS
Qy	2229 OKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELSAY 2278	RESULT 11	
qq	2417 ATVTELESGLRVNFNYATSLENKSTIQGFLHTYEYLLRQLSELSAEGINEDTQLSLV 2473	US-08-222-617A-12 ; Sequence 12, Application US	lication
0λ	2279 RYAAVVHV 2306	GENERAL INFORM	79 TION:
ΩP	2474 RPTENGDLHLPLAQSPLATTAEEQKVASLNQAFEREAFLAAEKIAVVQGDRALSYADLNG 2533	APPLICANT: APPLICANT:	Veenstra, Anr Martin, Juan
οy	2307 QANQL NQKSLGD LLKSSDAAIMAVSKIPFEIT 2338	APPLICANT: Ga APPLICANT: Gu	Garcia, Brund Gutierrez, Sa
qq	2534 QANQLARYIQSVSCIGADDGIALMLEKSIDTIICILAIWKAGAAYVPLDPTYPPGRVQLI 2593	APPLICANT: APPLICANT:	Von Doehren,
Qy	2339AFERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRV 2386	APPLICANT: APPLICANT:	Palissa, Harr Van Liempt, F
Db	2594 LEEIKAKAVLVHSSHASKCERHGAKVIAVDSPAIETAVSOOSAADLETIASLGNLAYI 2651	; APPLICANT: MO	: Montenegro, E

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VEQKAVLLLRDALRERYFGRDCTKHHGVLFLSNYVFDFSVEQLVLS 2711
                                                                                                                                                           | | : | : | : | : | : | PIXNAYGVTETTVYNIIAEFTTNSIFENALREVLPGTRAYVLTA-- 2829
                                                                                                                                                                                                         DRKELSRRAKVVPKQQTAAPLPT-----FPISEVEVILCEEATEV 2517
                                                                                                                                                                                                                                   QQPQLEYLGRGDLQIKMRGYRIEISEVQNVLTSSPGVREGAVVAKY 2943
                                                                                                                                                                                                                                                                                                                                         A----TKLISRID--ORLKVRITVKDVFDH------PVFADLA 2568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- 2407
                                                                 VADDEFYRMASTHGLSYLSGTPSLLQKIDLARLDHLQVVTAAGEEL 2771
                                                                                                                                         ------SYMIPSNI 2463
                                                                                                                                                                                                                                                                                                                                                                          LDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAEYSPF 2687
: ::|:|:|:|
WGCKITVRDIFEH----RTARALHDHVFMKDS------DRSNVTQF 3107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIKPQLELQEIIQDIYPSTQMQKAFLFDHTTARPRPFYTDFPS 2747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLVNHLDIFR-TVFAEASGELYQVVLSCLDLPIQVIETED-NINTA 2805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : |: | : | : | | : | | DLQQYHDVFRMRLKREEVGFVQSFAEDFSPAQLRVLNVKDVDGSAA 3205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGOGODRSAHMAPRIETEAILCDEFAKVLGFQ-VGITDNFFDLGGH 2627
                                                                                                                                                                                                                                                                                Eduardo P.
Method for Influencing Beta-Lactam
----DAVFHH----
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an F.
anc D.
Santiago
Sse L.
A. Hans
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471 FVRQTLMALVNGHLLAVINDVEKYDADTLLPFIRRHSITYLNGTASVLQEYDFSDCPSLN 530 746 TLVLVGEQMSSSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRAV-G 798 ::     :: : : :       ::	VVEATKRSGSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRISIP   1   1   1   1   1   1   1   1   1	VVKGDFLSYTLIPKSTHECPVEQSYSGRRWFLDQLDVGSLWYLIP :::	1235   MHHIISDGWSIDVLRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQ   1294	CMRINIDHHDTFGTLINOVKATTTAAFENBDIPFERV-VSALQPGSRDLSST : : :	
90 OX OX OX OX OX	9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	\$ 6 \$ 6 \$ 6	Qy Dp	60 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large; TITLE OF INVENTION: Quantities of ACV Synthetase NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS: ADDRESSE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive CITY: Chicago STREET: 111nois COUNTRY: USA 2 IP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	LITERATE STATE STA	STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Penicillium chrysogenum FEATURE: LOATION: 1366 OTHER INFORMATION: /label= region OTHER INFORMATION: /note= "Region of ACV Synthetase; aa 62-3727"	US-08-222-617A-12  Query Match  8.3%; Score 1341.5; DB 2; Length 3666; Best Local Similarity 21.2%; Pred. No. 1.16-107; Matches 730; Conservative 515; Mismatches 1232; Indels 963; Gaps 134;  Qy 312 FDKHYLADGTYQTVAPLRYHCOSNLRASDVMDAISSYDDRLGHLAPFGLRD1 363  Db 80 FSVHQMLKGFGNGTHTITASLHREQNLQNSSPSWVYSPTITYHENRDGWSVAQAVES1 137  Qy 364RNTGDNGSARCDFQTVLLYTGSHVNNGINGFLQOITESSHF-MPCNNRALLLHCQM 419	Db 138 EAARGSEKESVTAIDSASSLVKMGLFDLLVSFVDADDARIPCFDFPL 184  Qy	Db 241 AEGKQQLEEWNNTDGEYPSSKRLHHLIEEVVERHEDKIAVVCDERELTYGELNAQGNSIA 300 Qy 530 VHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDFPARTAQVVTQTRA 589 ::: : ::: ::: :: :: : : : :

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Qy	1744 CIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCV-DYMTTLDARALKDVFF 1798	OY 2387 EVSSAROWSONGA
qa	1536 SKVFGLRDTDDEVILS-FSNYVFDHFVEQMTDAILNGQTLLVLNDGMRGDKERLY 1589	Db 2591 IFTSGTSGKPKGV
Qy	AQGLYQGVQCYNG	QY 2408 CSQGRTLVNFPTD
qa		Db 2651 VLSGHKLIVPPAE
Qy		Oy 2445EVRER
qa	-	Db 2711 HATQYEKMRRRFN
Qy	ARGYSDKA-LDENREVHITVNDQTVKAYRTGDRVRYRIG-DGLIEFFGRM	Qy 2464 .VVLDKMPLNANGK
ପ୍		Db 2769 -ALQPVPFDAVG-
Qy	1967 DTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEIL-GFVVAD 2016	Oy 2518 F
qa		Db 2823 YKTGDLVRSRFNR
δō	2017 2033	Qy 2527HFNLGGHSL)
QO	1826 RFMQSRLPGYMVPSRLILVSKFPVTPSGKLDTKALPPAEEESEIDVVPPRSEIERSLCDI 1885	Db 2883 ENNDTYSRTAHSLY
Qy	2034 WQDHFES GMYS 2044	Qy 2569 SVIRGGLGLQDPVS
<b>q</b> a .	:     :   1886 WAELLEMHPEBIGIYSDFFSLGGDSLKSTKLSFMIHESFNRAVSVSALFCHRTVEAQTHL 1945	Db 2943 LDVRRLPEII
Qy		Qy 2628 SLMATKLAVRIGHE
qq		Db 2997 SITSLHLVAQIHNC
Oy	2082 TTRTLHDNRSLGN 2111	QY 2688 QLLFTEDPEEFMAS
qa	AKOVERL	:
δδ		QY 2748 TSEPDAAGLIKACE
qa	IV   	Db 3085 TPELDVDSLSAAVF
QY		Qy 2806 TNEFLDEFAK
qa	: ::    2121 ALQKTKSAANLPALKAQXKEYALYHRRQLSGDRMRNLSDFWLRKLIGLEPLQLITDRPRP 2180	Db 3145 VNEILDGWQSGFNL
Oy		OY 2862 LYNGRSLLPP
Db	VSVGIPV	Db 3203 LYRNGSLGSKGSSF
δō	2158DLHPDLVVLNSVIQYFPSSEYLAEIADTLIHL 2189	Qy 2917 CKALHLSKIVNIPS
qq	DMPFQEVTK	Db 3255 GSRVRLSRSLS-PE
ογ	2190PNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVR 2228	QY : 2976 PVEYQDIVGPCTNA
qa	: QYRPVQPVDSVAKFDLN	Db 3295 ALQHIAPTGPSM
δλ	2229 OKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELSAY 2278	RESULT 12
QQ	2356 ATVTELESGLRVNFNYATSLENKSTIQGFLHTYEYLLRQLSELSAEGINEDTQLSLV 2412	US-08-510-646B-33
Qy	2279 RYAAVVHV 2306	; Patent No. 6077699; GENERAL INFORMATION:
qa	:  -    :	APPLICANT: Blanc, Vero
Qy	2307 QANQL NQKSLGDLLKSSDAAIMAVSKIPFEIT 2338	Crouzet, Jacques,
q	2473 QANQLARXIQSVSCIGADDGIALMLEKSIDTIICILAIWRAGAAYVPLDPTYPPGRVQLI 2532	: Lacroix, : Thibaut,
Qy	;	
qq	2533 LEEIKAKAVLVHSSHASKCERHGAKVIAVDSPAIETAVSQQSAADLPTIASLGNLAYI 2590	; APPLICANT: De Crecy-Lac ; TITLE OF INVENTION: PO

7 EVSSAROWSQNGALC 2407	26	8 CSQGRTLVNFPTD 2444	1 VLSGHKLIVPPABEVADDEFYRMASTHGLSYLSGTPSLLQKIDLARLDHLQVVTAAGEEL 2710	EVRER	SIFENALREVLPGTRAY	4 :VVLDKMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCEEATEV 2517   :  :  :  ::   ::   ::   ::   ::   :	F	VQNVLTSSPGVREGAVVAKY 28	HFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLA 2568	ENNDTYSRTAHSLVGYYTTDNETVSEADILTFWKARLPTYMVPSHLCCLEGALPVTINGK 2942	SVIRQCLGLQQPVSDCQGQDRSAHMAPRTETEAILCDEFAKVLGFQ-VGITD	J	SLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAEYSPF 268		QLLFTEDPEEFMASEIKPQLELQEIQDIYPSTQMQKAFLFDHTTARPRPFVPFYIDFPS 2747 :	TSEPDAAGLIKACESLVNHLDIFR-TVFARASGELXOXVISCIDIPIONIETER-NIMTA OOO		TNEFLDEFAKEPVRLGHPLIRFTIIKQTKSMRVIMRISHALYDGLSLEHVVRKLHM 2861	33	LYNGRSLLPPHQ	LYRNGSLGSKGSSFRQWAEAIQNYKASDSERNHWNKLVMETASSISALPTST 3254	CKALHLSKIVNIPSQVLRGSSNIITQATVFNAACALVLSRESDSKDV-VFGRIVSGRQGL 2975	GSRVRLSRSLS-PEKTASLIQGGIDRQDVSVVDSLLTS-VGL 3294	PVEYQDIVGPCTNAVPVRAH 2995	:::     :   :   ALQHIAPTGPSMVTIEGH 3312	46B-33 34, Application US/08510646B 6077699 INFORMATION: ANT: Blanche, Francis ANT: Crouzet, Joel ANT: Crouzet, Joel ANT: Lacroix, Particia ANT: Thibaut, Denis ANT: Tagorec, Monique ANT: The Debussche, Lauren ANT: Depussche, Lauren ANT: Depussche, Lauren ANT: Depussche, Lauren ANT: Depusschen, Lauren ANT: Depusschen, Lauren ANT: Depusschen, Lauren ANT: Bebusschen,
. 238.	259	240	265	4		2464	2518	2823	2527	2883	9	2943	2628	1004	3047	2748	3085	2806	3145	2862	3203	2917	3255	2976	3295	1.2 510-6 510-6 ence nt No PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC PPLIC
Qy	QQ	Οy	qa	δο :	qq	oy Db	οy	QQ	QY	qq	Οy	οp	ð 2	3	Oy Dp	Οy	QΩ	οy	Db	Qy	qq	Οy	qa	Qγ	qq	RESULT US-08- US-08- Sequence Pate A A A A A A A A A A A A A A A A A A A

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1762 FDGASYEIYSALLFGRTLV 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09335409 Patent No. 6121029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Sorangium cellulosum US-09-335-409-3
                    1479 AYTRFDMEFHLFQETD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1410
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Best Local S.
Matches 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1188 IDLCGSDLDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDV 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1248 LRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQE------KQLNYWKK 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1301 OLKDS-SPAKIPTDFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFR 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1360 AAHYRLTAVEDAVIGTPIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATT 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1420 TAAFENEDIPFERVVSALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSK- 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1068 VGMDLKVSNIYQHPTLAGISAVVKGDPLSYTLIPKSTHEGPVEQSYSQGRLWFLDQLDVG 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 VVVPADEAGLAEMLAEAARHEFDVTSEPPLRVSLFTLAPDEHVLLLLLHHIAGDGWSLAP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Gaps
TITLE OF INVENTION: Coding For These Polypeptides And Their Use NUMBER OF SEQUENCES: 45
                                                E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 739;
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                                                                                                                                                                                                           : PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03806.0054-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 5.3%; Score 855; Similarity 31.0%; Pred. No. 4
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US (08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
                                                                                                                                                                                                                                                                                                                                                        PCT/FR 93/00923
                                                                                                                                                                                                                                         US/08/510,646B
                                                                                                                                                                             IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      FR 92/11441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 739 amino acids
amino acid
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                NUMBER OF SEQUENCES: 4:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                            CITY: Washington
                                                                                                                           20005-3315
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                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                              MEDIUM TYPE:
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                                                                                                            COUNTRY:
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1591 YTELDRQSDILAGWLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSA 1650
--SLKGSVNFADELFKMETVENVVRVFFEILRNGLQSSRTP 1533
                                                                                                                                       VSILPLTDGIVTLEKLDVLNVKHVDYPR---ESSLADVFQTQVSAYPDSLAVVDSSCRLT 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1708 P-SATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIP----NYPSETRMAHMATIA 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                            1651 RVQDILSGLSGPTIVLIGHDTA---PPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTK 1707
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                                                               420 GFAKFDLALAVAEERHADGRRSLRGDWEFSTDLFEQATVEALGARLTALLASVAADPDQP 479
                                                                                                                                                                                                                                                                                                                       77 IQESYWLGR-----TGA--FTVPSGIHAYREYDCTDLDVPRLSRAFRKVVARHDMLR 126
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                                                                                                                                                                                    480 IGRVGILD---PAERHRILHTWN-DTSRPGADATWPELFQARAAEHPDAVALVQEGTETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                596 RIAYLLQD-GAPALVLTHTSVAAGLPGGVPQLLVDQVGLDD-----VPGHDLTDAERTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCOMATION:
GENERAL INCOMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Gorlanch, Joern
APPLICANT: Gorlanch, Joern
APPLICANT: Gorlanch, Joern
TILE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICANT: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEO ID NOS: 30
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llarity 23.4%; Pred. No. 4.6e-59;
Conservative 247; Mismatches 597;
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qq	344 VHPRVNDITGDFTSMVLLDIDTTRDKSFEQRAKRIQEQLWEAMDHCDVSGIEVQREAARV 403	¥27T
Qy	1435 SALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYT-RFDMEFHLFQ 1491	Qy 2446 VRE
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Qy	1604 WLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVODILSG 1658	RESULT 14
qq	:       :   :      :	-10: e 3
ογ	VTNVEFVRIRDALNDSNA	Patent No. 6 GENERAL INFC
ф	624 VLTQPWLDGKLSWPPGIQRLLVSEAGVEGDGDQPPMMPIQTPS 666	
δy	1712 SLAYVLYISGSTGRPKGVMIEHRVIRTVTSGCIPNYPSETRMAHMATIAFDG 1764	
qq	667 DLAYVIYTSGSTGLFKGVMIDHRGAVNTILDINERFEIGPGD-RVLALSSLSFDL 720	APPLICANT: APPLICANT:
οy	YSALLFGRT	
QQ	721 SYYDVEGILAAGGTIVVPDASKLRDPAHWAELIEREKYTVWNSVPALRMLVEHF 775	
δō	1820PRRLSRILMFFFLVVTDSTAPDALDAQGLYQCVQCYNGYGPTENGVMSTIYPIDS 1874	; PRIOR APPLICAT ; PRIOR FILING D
qq	776 EGRPDSLARSLRSGDWIPVGLPGELQAIRPGVSVISLGGATEASIWSIGYPVRN 833	; NUMBER OF SEQ ; SOFTWARE: Pate
Qy	1875 TESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGY SDKALDENRF 1932	; SEQ ID NO 3 ; LENGTH: 1410
QQ	) SEALEPRPVWVPG	; TIPE: PKT ; ORGANISM: SOI
οy	1933 VHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSV 1992	5-70T-89C-60-SD
Dp	894 VHPETGERLYKTGDLGRY-LPDGNIEFMGREDNQIKLRGYRVELGEIEETLKSHPNV 949	a t
Qy	7LQQNEDQAPEILGFVVADHDHSENDKGQ	Matches 374
qq	950 RDAVIVPVGNDAANKLLLAXVVPEGTRRRAAEQDASLKTERIDAR 994	
Qy	2053 TIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLHDNRSLGNVLEIGTGSGMILFNLDSR 2112	. Db 77 IQE
qq	995 AHAAEADGLSDGERVQFKLARHGLRRDLDGKPVVDLTGQ 1033	Oy 1164 T-T
Qy	2113 LESYVGLEPSRSAAAFVNKATESIPSLAGKAKV 2145	Db 127 AHT
Ωp		Qy 1211 LSS
Qy	2146 QVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVRSQAT 2205	Db 182
<b>q</b> O	1094 QTYAYVKSGRIEGVDEGFYYYHPFEHRLLKLSD1126	Qy 1267 LSA
Oy	2206 NEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEIL 2265	· Db 225 ETS
qq	1127	QY . 1325 GCV
Qy	2266 PKNMEAVNELSAYRYAAVVHVRGSLĠDELVLPVEKDDWIDFQANQLNQKSLGDLLKSSDA 2325	Db 284 RFR
qa		Oy 1381 NRP
Qy	2326 AIMAVSKIPFEITAFERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFR 2385	344 VHP
qa		Qy 1435 SAL
QY	GALDAVFHHCCSQGRTLVNFPTDHHLRGSDLLTNRPLORLONRRIAIE	Db 404 LGI

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2502
                                                                  SEVEVILCEEATEVFGMK-VDITDHFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDH 2561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEV------LNQEQTTPFN 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHVT--IDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANR-- 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTPLPIQYSDF -- AKWQKDQFIEQEKQLNYWKKQLKDSSPAKIPTDFARPALLSGDA 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERV-----V 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQPGS--RDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYT-RFDMEFHLFQ 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : |: |: : : | TLPDM----MQVIEPRVDADIEIIDLRGLDRSTREARLVSLRDAMSHRIYDTERPPL- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHTEQWLPSDSWGRLKRRVGERGLTPTGVILAAFSEVIGRWSASPRFTLNITLFNRLP 343
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nilarity 23.4%; Pred. No. 4.6e-59;
Conservative 247; Mismatches 597; Indels 379;
                                                                                                                                                                                                                                                                                                                                                                                                                VFADLASVIRQGLGLQQPVSDGQGQDRSAHMAPRTE 2598
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Ligon, James
Molnar, Istvan
Zirkle, Ross
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Search completed: May 30, 2003, 12:50:06 Job time: 83 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 30, 2003, 12:48:42; Search time 85 Seconds Run on:

(without alignments) 3726.223 Million cell updates/sec

US-09-482-788-2 16128 1 MEYLTAVDGRQDLPPTPASF.....RVEHLLEEVSKTFEGLNSSL 3129 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

383519 segs, 101223694 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

/cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep

/cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/USO6\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep

ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*/ptodata/1/pubpaa/US09\_PUBCOMB.pep: /ptodata/1/pubpaa/US10\_NEW\_PUB.pep: /ptodata/1/pubpaa/US10\_PUBCOMB.pep: /cgn2\_6/p /cgn2\_6/ /cgn2\_6/ /cgn2\_6,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

## SUMMARIES

Description	Sequence 11870, A	Sequence 5107. Ap	Sequence 15, Appl	Sequence 12265. A	Sequence 14, Appl	Sequence 5654, Ap	Sequence 3, Appli	Sequence 13, Appl	Sequence 44. Appl	Sequence 10079, A	Sequence 13724, A	Sequence 18, Appl	Sequence 4, Appli	Sequence 8, Appli	Sequence 6480, Ap	Sequence 88, Appl	Sequence 5301, Ap	Sequence 12515, A	Sequence 86, Appl
ID	US-09-815-242-11870	US-09-815-242-5107	US-09-976-059-15	US-09-815-242-12265	US-09-976-059-14	US-09-815-242-5654	US-10-014-717-3	US-09-976-059-13	US-10-166-087-44	US-09-815-242-10079	US-09-815-242-13724	US-09-976-059-18	US-10-008-016-4	US-09-994-595-8	US-09-738-626-6480	US-09-924-256A-88	US-09-815-242-5301	US-09-815-242-12515	US-09-924-256A-86
	10	10	6	10	6	10	6	6	6	10	10	6	6	6	6	10	10	10	10
Query Match Length DB	2448	4342	4999	2397	4999	1668	1410	1051	1446	1293	1294	891	458	1391	1295	401	485	485	399
Query Match	10.6	10.4	10.1	8.7	8.5	8.5	4.9	3.9	3.8	3.5	3.3	2.9	2.9	2.7	2.6	2.6	2.4	2.4	2.4
Score	1713.5	. 1677	1632	1406	1375.5	1374	782.5	623	612.5	559	538.5	475.5	463	434.5	424	415.5	390	390	379.5
Result No.	-	2	33	4	S	φ	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 10589, A Sequence 82, Appl	Seguence 24, Appl	Sequence 11698, A	Sequence 18, Appl	Sequence 42, Appl	Sequence 84, Appl	Sequence 92, Appl	Sequence 13644, A	Sequence 56, Appl	Sequence 3950, Ap	Sequence 90, Appl	Sequence 3817, Ap		Sequence 10, Appl	Sequence 19, Appl	Sequence 19, Appl	Sequence 3, Appli	Sequence 31, Appl	Sequence 24, Appl		Sequence 23, Appl	Sequence 16, Appl	Sequence 44, Appl	Sequence 25, Appl	
US-09-815-242-10589 US-09-924-256A-82	US-09-924-256A-24 US-09-924-256A-94	US-09-815-242-11698	US-09-924-256A-18	US-10-166-087-42	US-09-924-256A-84	US-09-924-256A-92	US-09-815-242-13644	US-10-169-048-56	US-09-738-626-3950	US-09-924-256A-90	US-09-738-626-3817	US-09-947-027-10	US-10-091-009-10	US-09-906-419-19	US-10-119-136-19	US-10-149-485-3	US-09-838-469-31	US-09-838-469-24	US-09-838-469-15	US-09-838-469-23	US-09-838-469-16	US-09-836-705-44	US-09-838-469-25	
10	10	10	10	6	10	10	10	6	6	10	σ	10	12	σ	6	σ	σ	5	σ	6	σ	6	6	
506 390	392 388	471	390	9	396	392	516	512	568	396	512	532	535	722	722	491	550	544	546	546	546	3032	547	
2.3	2.3	2.3	2.3	2.3	2.5	2.2	2.1	2.1	1.9	1.8	1.7	1.6	1.6	1.5	1.5	1.5	1.4	1.4	1.4	1.4	1.4	1.4	1.4	
379.5	376 369	369	366.5	363.5	352.5	347.5	346.5	334.5	311	284.5	277	256	256	237	237	236.5	233.5	232	231	231	230	229.5	228	
20	22 23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/204,578
PRIOR APPLICATION NUMBER: 60/225
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-16
PRIOR SEQ. ID NOS: 14110
SOFTWARR: FASSEQ for Windows Version 4.0 Sequence 11870, Application US/09815242 Patent No. US20020061569A1 Pseudomonas aeruginosa GENERAL INFORMATION: APPLICANT: Haselbec RESULT 1 US-09-815-242-11870 SEQ ID NO 11870 TYPE: PRT ORGANISM:

DB 10; Length 2448; Score 1713.5; DB 10 Pred. No. 2.4e-115; 10.6%; 28.6%; Query Match Best Local Similarity US-09-815-242-11870

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385;	-IESWN	TLSEWN	SLGLRA	:  :   ARGVGAI	ALTSKLI	LLTQGH	IMIEH-	TLLTHR	QWVSRSI	GEQMSS	: GEALDL(	NNMGRAVGAHSWVIDP	STIPDES	PANTEPDGAKLYR	3EV3/V/1	:    :  SVRDAV	SFYICM	HLMLLE	WQSLGI	:   : VSEILGV	/KGDPLS	:: ERTTDA	RALAALE	: :  RSFDSLV	NOEQTT	ERIQAIVVQPFDLE	DSKDPL	MCTDVV	LLSGDA	, RQSHRG	NRNRPE	NRNRVE	PGSRDL:    : P-ERNA:	ביימים ב
Indels	YDHNVIDSLOTTRLLQOFGHLIK-CLQSPLDLSSMAEVNLMTEYDRAE-IESWNSQPLE	YATDLFDASTVERLAGHWRNLLRGIVANPRORLGELPLLDAPERROTLSEWNPAGREC	-VODTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIP		YFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVALTSKLHRETVQ 	VGLALERSLDMLVGLLAILKAGGAYLPLDPAAPEERLAHILDDSGVRLLLTQGHLLERLP	KLVG-RCVVVDDELLQSVSASDDFSSLTKSQDLAYVIFTSGSTGDDKGIMIEHRAF	TGRPRG	SSCALKEGASLGINSTITALCEGTHAFGACLLEIMTTLINGGCVCIPSDDDR  LI	PGLATLVLVGEQMSSSVNAIW	:     :     :     :   -   :   :     :     :     :   :     :   :     :   :     :	FASNMSTEPNNMGRAVGAHSWVIDP	LVSPIG	NDINKLVPIGAVGELVIESPGIARDXIVPPPPEKSPFFTDIPSMYPANTFPDGAKLYR 	יי בינתחם אני	TGDLARFQADGNIEYIGRIDHQVKVRGFRIELGEIEAALAGLAGVRDAVVLAHDG	ANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRT		AKLHSI	VNGKLDRQALPQPDASLSQQAYRAPGSELEQRIAAIWSEILGVERV	NVGATFFELGGNSITAIKMVNMAR-SVGMDLKVSNIYQHPTLAGISAVVKGDPLSYTLIP	: :     : : : : : : : : : : : : : : : :	NVDALRI	. :  :	-EDQDGÖGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLS	ER]	SEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDLNQLYSAALKDSKDPLSALTP	LY-AAYS	TDFARP	LPIQYADYALWQRSWMEAGEKERQLAYWTGLLGGEQPVLELPFDRPRPARQSHRGAQLGF	TIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDII	RVGVPIP	GCEVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGSRDLSSTPL	77777777
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tches	PLDLSSN	PRQRI	SDWTYSE	:    ORLSYGE	OPNDPPA	PAAPEE	(SQDLAY	ADNUAL	ACLLEIM : [] SSVWEIF	MNSIPSFINRYNVNWMMATPSYMGTFSPEDV	: /ACSADM	-QLLNGYGQSESSICFASNMSTEP	TIRPVS	PPPEKS	VELGAT	:	ATKAIN	::: -RESLR	A-PAPI	AYRAP-	DLKVSN	DASLKAI	YLIPYA	 YHIPSAI	SEEMKV1	LRTRERLEGGRSYQQVQPAVSVSIEREQFGEEGLI	GWSIDVI	GWSMQVP	KQLKDSS	SLLGGEQ	RAAHYRI	QALLYRY	FTAAFEN   : ALEAQAH	X
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ervative	OTTRLLC	FVERLAC	EMLKAVS	: RFEEQAF	VIASMI	MLVGLL	YDDELLO		ilginsd    ERD	YNVNW	: EGVTVL	LLNGYG	DIENNAT	AVGELV 	GSIVCL	GNIEYI	IGSSYF	: l VADS	RIMGKD	1	GNSITA	GHSLLA	SYSOGRI	I::    SFAQER(	EDC	RSYQQVC	REGEDDA	CAEDDE	VOKDC	VQRSWME	RAFCNE	RALAQRE	INIDHHE::/ adederm	
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RESULT 2 US-09-815-242-5107 : Sequence 5107, Application US/09815242

. F	SS20020061569Al DRMATION: Haselbeck, Robert	Oy Db	458 LDLSSMAEVNLMTEYDRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTAIQAWD-GDW 516 ::   :
	Onisen, kari L. 29skind, Judith W. Wall, Daniel Trawick, John D.	Qy	517 TYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDP 576
APPLICANT: Carr, APPLICANT: Yamamo APPLICANT: Xu, H. TITLE OF INVENTION	APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes in	δy da	577 PARTAQVVTQTRATVALISKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLIKSQDLA 636
TITLE OF INVENTION: PROKAR, FILE REFERENCE: ELITRA 011A CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-	TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.0111 CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21	\rangle \rang	637 YVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALOFGTHAFGACLLEIMTTL 696
PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2000-05-23	PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23	QQ Dp	697 INGGCVCIPSDDDRMNSIPSFINRYNVNMMMATPSYMGTFSPEDVPGLATL 747 :
	APPLICATION NUMBER: 60/20/,/2/ APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23	QV do	748 VLVGEQMSSSV-NAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRAVGA 799
	00/23,625 2000-11-27 NUMBER: 60/257,931 2000-12-22	Qy	800 HSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDG 859   1409 VVCRVLDABEN-LLPAGVAGELCIGGLGLARGYLGRPALSAERFVADPFSAAG 1500
PRIOR PILING DATE: 200/102-16; NUMBER OF SEQ ID NOS: 11110; SOFTWARE: FastSEQ for Windows	FRICK APPLICATION WOMBER: 0V/A09,308 PRIOR FILING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 14110 SOFTWARE: FastSEQ for Windows Version 4.0	da .	860 AKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIVVEA 917   :
; SEQ 1D NO 510/ ; EEQ TH: 4342 ; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa	nonas aeruginosa	Qy Dp	918 TKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICM 977
Simi	10.4%; Score 1677; DB 10; Length 4342; Larity 23.6%; Pred. No. 38-112; Concervative Alor Mismarches 1781; Indale 852; Cars 135.	δλ Dp	978 LELPRTATGKIDRRKLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLH 1028 ::
		Qy	1029 SIWYQSLGIDPATVNYGATFFELGGNSITAIKMYNMAR-SVGMDLKVSNIYQHPTLAGI- 1086 :  :  :  :  :  :  :  :  :  :  :  :  :
	090 IDFQS ANINIFGGURLROBEDBEAALRASEORLVERHEALRIFRE LERGGAALLGRIDE 745  119 KDSFVFSWMCWSSSSPDEVVRDEAAAAASGPRCNRFVLLEDMQTK 164  11	δγ	1087SAVVKGDPLSYTLIPKSTHEGEVEQSYSOGRLWFLDQLDVGSLWYLIPYAVRMRCP 1142 
		Qy	1143 VNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFE 1199 1::
192		Qy	1200VLNQEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDLNQLYS 1257 :::
243 243 017		Qy Db	1258 AALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSP-AKIPTDF 1314
		Qy	1315 ARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIG 1374
347	AQANQDLEFEDQVLAACGQGGQLEQVLENHQQRDLSALR IRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFM	VQ OY	1375 TPIANRNEPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVV 1434 
407	ı Q	Qy	1435 SALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTRFDMEF 1487
Db 1053	LOSEEDARGRLTLNFDYAADLFDEASIRRFAAQYLELLRQVAEDPQRCL 1101	٥٧	1488 HLFQETDSLKGSVNFADELFKMETVENVRVFFEILRNGLQSSRTPVSILPLTDGIVTLE 1547

Db 3015 LLQQAPAAYRTQVNDLLLTALARVLCRWSGQPSTLVQLEGHGREALFDDIDLTRSVGWFT 307	QY 2468KMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTFPISE 250  DS 3075 SAYPLRLTPAQSPGE-SIKAIKEQLRAVPHKGLGYGVLRYLADPAVRQAMAALPTAPIT- 313	Qy 2506 VEVILCEEATEVFGMKVDITDHFPNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFA 2565	OY 2566 DLASVIRQGLGLQOPVSDGQQDRSAHMAPRTETEAILCDEFAKVLGFQVGITDNFFDLG 2625  DD 3145 DALFOPLDQPTGPIHDEQAPLPNELSVDGQVYG 3177	Oy : 2626 GHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREM 2681  Db :	QY 2682 AEYSPFQLLFTEDPEEEWASE1-KPQLELQE1IQDIYPSTQMQKAFLFDHTTARPR 2736   1   1   1   1   1   1   1   1   1   1	QY 2737 PFVPFYIDFPSTSEPDAAGLIKACESLVNHLDIFRTVFAEASGE-LYQVVLSCLD 2790  1	QY 2791 LPIQVIETEDNINTATNEFLDEFAKEPVRLGHPLIRETIIKQTKSMRVIMRISHALYDGL 2850	Oy 2851 SLEHVVRKLHMLYNGRSLL	QY 2884 GRESGHGFWRDVIQNTPWTILSDDTVVDGNDATCKALHLSKIVNIP 2929	Qy 2930 SQVLRGSSNIITQATVENAACALVLSRESDSKDVVFGRIVSGRQ-GLPVEYQDIVGPCTN 2988 1	OY 2989 AVPVRAHIESSDYNQLLHDIQDQYLLSLPHETIGFSDLKRNCTDWPEAITNFSCCI 3044 :::::::::::::::::::::::::::::::::::	OY 3045 TYHNFEYHPESQFEQORVEMGVLTKEVNIEMDEPLYDLAIAGEVEPDGAGL 3095	QY 3096 KUTVIAKTQLFGRKRVEHLLEEVSK 3120 S:                 Db 3649 HLSYDQRYFEAPTVERLLGEFKR 3671	RESULT 3 US-09-976-059-15 ; Sequence 15, Application US/09976059	: Patent No. US20020164747A1 ; GENERAL INFORMATION: ; APPLICANT: Farnet, Chris ; APPLICANT: Zazopoulos, Emmanuel	; APPLICANT: Staffa, Alfredo ; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin ; FILE REFERENCE: 3019-PCT ; CURRENT APPLICATION NUMBER: US/09/976,059	; CURRENT FILING DATE: 2001-10-15 ; NUMBER OF SEQ ID NOS: 34 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 15	LENGTH: 4999
EVTDLDQRLGCCLTYSRDLFDEPRIARWAGHWQNLLEALLGDPQRRIAELDLFAAEE 2169	KLDVIAVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAG 1603 : :	SGLSG	$\omega - \omega$				ALDEN     ALSAE			NRSLGNVLEIGTGSGMILF 210	QVGTATDIGQVDDLHPDLVVL	VRSQATNEHF-  ::    2VVSRARQLGIHFS	EELLV 22 :   : QALLL 28	EPAFFISLKDRFPGLVEHVEILPKNME-AVNELSAYRYAAVVHVRGSLGDELV 2295 :	LPVEK-DDWIDFQANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAFERQVVASL 2348 :  :	NSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSARQWSQNGA 2399 : :	2400 LDAVFHHCCSQGRTLVNFPTDHHLRGSDLLTNRPLQ 2435   1   1   1   1   1   2959 LQAYAGSESLREELGWWQARLGGQPVEWPCDRP-QGDNREALAESVSLRLDPQRTRQ 3014	

ò	1962 FEGRMDTOFKIRGHRIESABIEAALIRDSSVRDAAVVIGONEDGABETIGEVVARURGES 2021	
oda da		Db 3513 TGLRDQLAGLLVHEHAPLALAQRAAGITDGSPLFASIFNYRHNQDDPAASAGLE 3566
Võ	2022 NDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGE 2081	3064 MGVLTKFVNIEMDEPLYDLAIAGEVEPDGAGLKVTVIA 31
QQ	3023 3026	DD 3567 -GIRTVYSAEHTNYPL-DASIDVTGDRFAITVNAVA 3600
οy	2082 TTRTLHDNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEPSRSAAAFVNKATESIPSLAG 2141	RESULT 4
qq	3027 3034	US-09-815-242-12265 ; Sequence 12265, Application US/09815242
οy	2142 KAKVQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVR 2201	; Patent No. US20020061569A1 ; GENERAL INFORMATION:
Dp	3035VGGDA- 3039	: Haselbeck, Robert : Ohlsen, Kari L.
οy	2202 SQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRFPGLVEH 2261	
OD	3040 3039	; APPLICANT: Trawick, John D. ; APPLICANT: Carr, Grant J.
.vo	2262 VEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLK 2321	; APPLICANT: Yamamoto, Robert T. ; APPLICANT: Xu, H. Howard
QQ	3040 3039	; TITLE OF INVENTION: Identification of Essential Genes in ; TITLE OF INVENTION: Prokaryotes
Qy	2322 SSDAAIMAVSKIPFEITAFERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGE 2381	; FILE REFERENCE: ELITRA.011A; CURRENT APPLICATION NUMBER: US/09/815,242
qq	3040 3047	A A
٥y	2382 AGFRVEVSSARQWSQNGALDAVFHHCCSQGRTLVNFPTDHHLRGSDLLTNRPLQRLQNRR 2441	FILING DATE: 2000-03-21 APPLICATION NUMBER: 60/206,84
qq	3048308 3049	2000-05-23 NUMBER: 60/207 72
٥y	PLPTF	FILING DATE: 2000-05
qq		FILLICATION NOMBOL. 00/242/3/ FILLION DATE: 2000-10-23 PDDITCATION NIMBED: 60/363 63
οy	ISRIDORLKVRITVKDVFDH	FILING DATE: 2000-11 APPLICATION NUMBER:
QQ		FILING DATE: 2000-12-22 APPLICATION NUMBER: 60/269
Qy	2562 PVFADLASVIRQGLGLQQPVSDGQGQDRSAHMAPRTETEAILCDEFAKVLGFO-VGITDN 2620	FILING DATE: 2001-02-16
Dp		RE: FastSEQ for NO 12265
0y		LENGTH: 2397
Dp		, TrE. FAI ; ORGANISM: Staphylococcus aureus US-09-815-242-12265
οy	2681 WÁEYSPPQLLFTEDPEEFWASEIKPQLELQEI1QDIYPSTQ 2721	= 1406;
qq	3165 GAVVVPPNLIPEDAAELTPEMLPLADLTADELAVVVASVPGGAANIADVYPLAP 3218	LOCAL SIMILATILY 24:24; FIEU. NO. nes 571; Conservative 394; Mismatc
ΟŊ		QY 212 DTDSQSVSVVSMSCEDNAVSATHFWQTHLNDLNASVFPHLSDHLMVPNPTTTAEHRITFP 271
Q C		Db 176 DKDNQDASHIALDSNYFRLEKNSDIHIDSYLPIKHPFEQALYQ-TYL 221
oy Db	2777 ASGELYQVVLSCLDLPIQVIETEDNINTATNEFLDEFAKEPVRLGH-PLIRFTIIKQTKS 2835	LADGTYQTVAPLR 32
è	WD UTMD1cuni vpct ct bundibut tutt valen - 170 - 100 - 1	MISIDMASLAVSVILANHIMSUQHDVILGIHVPSHLPNDLH
g G	3335 GRWLALLRIHHLVQDHTTLDVLLGELRAFLEGRGDELPEPVPFREFVAQARLGVPREEHE 3394	QY         330 VHCQSNLRASDVMDAISSYDDRLGHLAPFGLRDIRNTGDNGSAACDFQTVLLVTDGSH 387           :       :     :     :     :       :       :
٥y	2890 GFWRDVION-TPMTILSDDTVVDGNDATCKALHLSKIVNIPSQVLRGSSNI-ITQATV 2945	QY 388 VNNGINGFLQQITESSH-FMPCNNRALLLHCQMESSGALLVAYYDHNV 434
qq	3395 RYFABLIGDVIETTAPYGLTEVHGDGSAAVHSRREVDDDLAARLHRLARSLGVSPAAL 3452	KIIYNSAA
Qy Ph	FNAACALVLSRESDSKDVVFGRIVSGROGLPVEXQDIVGPCTNAVPVRAHIESSDYNQLL	435IDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEYDR :           :: ::   :
a ;		360 YDL
ζ	3006 HDIQDQYLLSLPHETIGFSDLKRNCTDWPEAITNFSCCITYHNFEYHPESQFEQQRVE 3063	Qy 490TLIHHEMLKAVSHSPTKTAIQAWDGDW-TYSELDNVSSRLAVHIKSLGLRAQQAI 543

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VGSLWYLIPYAVRMRGPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEM 1185
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                                              KVIDLCGSDLDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSI
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Patent No. US20020061569A1
GENERAL INFORMATION:
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REPERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                        Length 4999;
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Similarity 28.0%;
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### APPLICANT: Yanmanoto, Robert T.  #### PERCENTER, X.M. H. Movat (incline) of Essential Genes in Fift Co. INVESTION: Essential Content of Essential Genes in Fift Co. INVESTION: Essential Content of Content o	OY 1023 TAAKLHSIWVQSLGIDPATVNVGATFFELGGNSITAIKMVN-MARSVGMÖLKVSNIYOHP 1081	1   1   1   1   1   1   1   1   1   1	1429   PFERVUSALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFGGLESVPVPSKAYTRFD   1484   1486   1486   1486   1486   1486   1488	1661 GPTIVLIGHDTAPPDIEVTHVE-FVRIRDALNDSNADGFE  1190 VTAVMSYGIELETTLPVIQLENAKGFVESKENEGYDDLHGDQLENTA  1713 LAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETRMA  1242 -MAIYTSGTTGMPKGVAIRQRNLLNLVHA	VETGRALINGS AT VUPPAQUE OLONGO CHARACTER STRANDENT VALEAGINGS AND CHARACTER STRANDENT VALEAGINGS AND CHARACTER STRANDENT VALEAGINGS CONTROL STRANDENT VALEAGINGS CONTROL STRANDENT VALEAGINGS CONTROL STRANDENT VALEAGINGS CONTROL CON
on of Essential Genes in  9/815,242  7078  848  727  727  727  728  625  931  Core 1374; DB 10; Length 1668; red. No. 7.98-91; Indels 246; G Mismatches 683; Indels 246; G Mismatches 683; Indels 246; G SOPLEVODTLIHHEMIKAVSHESPTKTA  :	\to \to \to \to \to \to \to \to \to \to	40 40 40 60 70 70 70	62; • 88 88 566 143	684 256 742 316 792 373 427	909 472 962 517 1022 565
70 · ~~~~	ential Genes	PAPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22 APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16 R OF SEQ ID NOS: 14110 AND SEQ ID NOS: 14110 AND 5654 TH: 1668 TH: 1668 NISM: Staphylococcus aureus NISM: Staphylococcus aureus	Best Local Similarity   27.3%;   Score 1374;   DB 10;   Length 1668;     Best Local Similarity   27.3%;   Pred. No. 7.9e-91;     Matches   459;   Conservative   292;   Mismatches   683;   Indels   246;   Ga     461   SSMAEVNLMTEYDRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTA.		WYPANTEPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQ :  :  :  :  :  :  :  :  :  :  :  :  :

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1712 SLAYVLYTSGSTGRPKGVMIEHRVIIRTVTS-----GCIPNYPSETRMAHMATIAFDG 1764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-976-059-13
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                                                                                                                                                                                    APPLICANT: Cyr, Devon
APPLICANT: Goetlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.9%; Score 782.5; DB 9;
Best Local Similarity 23.4%; Pred. No. 9.7e-48;
Matches 374; Conservative 247; Mismatches 597;
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/014,717
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                      Sequence 3, Application US/10014717
Publication No. US20020192778A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Sorangium cellulosum
US-10-014-717-3
                                                                     GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Isrvan
APPLICANT: Zirkle, Ross
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1875 TESFINGVPIGRALNNSGÄYVVDPEQQLVGIGVMGELVVTGDGLARGY--SDKALDENRF 1932
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                                                                                                  1765 ASYEIYSALLFGRTLVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVPLRV----
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                                                                                                                                                                                                                                          1820 ---PRRLSRTLMFFFLVVTDSTAPDAL--DAQGLYQGVQCYNGYGPTENGVMSTIYPIDS
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APPLICANT: Zazopoulos, Emmi
APPLICANT: Staffa, Alfredo
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APPLICANT: Ecopia Blosciences Inc.
APPLICANT: Staffat
APPLICANT: Staffat
APPLICANT: Staffat
APPLICANT: Azapoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
FILE REFERENCE: 3104-202
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.0
SEQ ID NO 44
                         -LYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYV
                                            VDPEQQLVGIGVMGELVVTGDGLARGYSDKA-LDENRFV--HITVNDQTVKAYRTGDRVR
                                                                                                                      1953 YRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGF
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Publication No. US20030077767A1
GENERAL INFORMATION:
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US-10-166-087-44
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OTHER INFORMATION: V represents a non-standard codon. It is expected that the biosy
OTHER INFORMATION: nthesized protein will have a formylmethionine residue at this pd
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TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin FILE REFERENCE: 3019-PCT CURRENT APPLICATION NUMBER: US/09/976,059 CURRENT FILING DATE: 2001-10-15 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin version 3.0 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.9%; Score 623; DB 9; Length 1051; Best Local Similarity 21.4%; Pred. No. 2.6e-36; Matches 328; Conservative 157; Mismatches 477; Indels 568;
                                                                                                                                             TYPE: PRT
ORGANISM: Actinoplanes
FEATURE:
                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)..(1)
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US-09-976-059-13
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                                                                             955 RALEARLADRAGIEPAGGGGMDWT---DCERAIADLWIEVLGHGPAIPDD----DFFEL
                                  GSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLHDNRSLGNVLEI
                                                                                                                                          GTGSGMILFNLD----SRLESYVGLEPSRSAAAFVNKATESIPSLAGKAKVQVGTAT-DI
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APPLICANT: Yangmoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: UNMERR. 105/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10079
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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APPLICANT: YSKING, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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                                                                                                                   Gaps
                                                                                                             Indels 177;
                                                      Length 1446;
                                                      Query Match 3.8%; Score 612.5; DB 9; Best Local Similarity 25.4%; Pred. No. 2.7e-35; Matches 293; Conservative 163; Mismatches 519;
US-10-166-087-44
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PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR PELING DATE: 2000-05-23 FRIOR PELING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/245,578 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-12-26 PRIOR FILING DATE: 2000-12-16 NUMBER OF SED ID NOS: 14110 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: RastSEQ for Windows Version 4.0 SQGANISM: salmonella typhi FEATURE: NAME/KEY: VARIANT COCATION: (1)(1294) CUS-09-815-242-13724	Query Match 3.3%; Score 538.5; DB 10; Length 1294; Best Local Similarity 24.5%; Pred. No. 5.6e-30; Matches 244; Conservative 142; Mismatches 428; Indels 183; Gaps 38;	QY 1114 SQGRLWFLDQL-DVGSLWYLIPYAVRMRGPVNVDALRRALAALEQRHETLRTTFEDQDG-1171	QY 1172 VGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNOEQTTPFNLSSEAGWR 1218	Qy 1219 ATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDLNOLYSAALKDŞKDPLSALTPLP- 1274 	QY 1275IQYSDFAKWQKDQFIEQEKQLNYWKQLKDSSPAKIPTDFARPA 1318	QY 1319 LLSGDAGCVHYTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIA 1378	QY 1379 NRNRPELEDIIGCEVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVYSA 1436	QY 1437 LQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTRFDMEFHLFQETDS1495	Db 390 LDIELLANÄQRYDDATLSRHALRLMALITQFADNPALRCGDAQMLLAEEQ 439  QY 1547 EKLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLR 1606  :	OY 1607 RRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVL 1666   :	Db 549EDAQPKLLITTXAQLARFHDIPGMEYLCYSQPLPVSDATPLGLSLPHHTAYI 600
1332 DGELYOSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDIIGC 1391  233 DGE-FROLATQLSGVORTDLALALAALWIGRICNRMDYAAGFIFMRRIGSAALTATGP 289  1392 FVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVYSALQPGSRDLSSTPLAQ 1451  290 VLNVLPIGIHLAQETLDELATRLAAOLKKMRRHORYDAEQIVRDSGRAAGDEPLEG 346  1452 LIFAVHSQKDIGFFKFQGLESPVPSKAYTRFDMEFHLFQETDSLKGSVNFA 1503  347 PVLNIKVFDYQ-LDIPDVQAQTHTLATGPVNDLELALFPDVHGDLSIEILA 396  1504DELFKMETVENVVRYFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKH 1556  151   1   1   1   1   1   1   1   1   1	1677 EVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVI 1736 1   1	1737 IRTUTSGCIDNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALK 1794 : :	1795 DVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFELVVTDSTAPD 1841	1842 ALDAOGLYQGVQCYNGYGPTENGVMSTIYPIDSTE-SFINGVPIGRALNNSG 1892 	1893 AYVVDPEQQLVGIGVMGELVVTGDGLARGYSDKA-LDENRFVHITVNDQTVKAYRTG 1948 	1949 DRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQN 2002 	2003 EDQAPEILGFVVA 2015   ::: :: : 899 GGDARQLVGYLVS 911	SULT 11 -09-815-242-13724 Sequence 13724, Application US/09815242 Patent No. US20020061569A1 EERRRAL INFORMATION:	APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Karl L. APPLICANT: 2/skind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick, John D.	APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert T. TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA OIL A	CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078

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991 RRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAA·······KLHSIWVQSLGID 1038
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                                                                                                                                                                                                                                                                                              931 AFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRTATGKIDR 990
    536 LAERGVTVLNQTPSSFTQLVAADRGAERDLAVRLVIFGGEPLDARTVLPWLDRRPEARCR 595
                                                                                                                                                                       656 GGAGVAIGYLNRPELTAERFVTG------PDGRRWYRSGDRGRLLPDGTLEHLGRL 705
                                                                                                                                                                                                                DSQVKIRGQRVEL------GAIETHLRQQMPDDLTIVVEATKRSQSANSTSLI 930
                                                                                                                                                                                                                                                                                                                                                                                                                      ------PEPARPAADAATPAGPGEDGLAGDLADVWQQVFG-- 836
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                                                                       768 LLNGYGQSESSSICFASNMSTEPNNMG-RAVG--AHSWVIDPNDINRL-VPIGAVGELVI
                                                                                                                             824 ESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLYRTGDLARYASDGSIVCLGRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1039 PATVNVGATFFELGGNSITAIKMVNMARSVGMD-LKVSNIYQHPTLAGISAVVK 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10008016
Facel No. US/2002013630A1
GENERAL INFORMATION:
APPLICANT: Mayers, Rachel A.
TITLE OF INVENTION: 33217, A NOVEL HUMAN AMP-BINDING ENZYME
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-110001
CURRENT APPLICATION NUMBER: US/10/008,016
CURRENT APPLICATION NUMBER: 60/246,669
PRIOR APPLICATION NUMBER: 60/246,669
PRIOR APPLICATION NUMBER: 60/260,669
PRIOR APPLICATION NUMBER: 60/260,11-08
PRIOR APPLICATION NUMBER: 60/260,166
PRIOR PRILING DATE: 2001-01-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.9%; Score 463; DB 9; Length 456 Best Local Similarity 33.1%; Pred. No. 3.1e-25; Matches 156; Conservative 68; Mismatches 171; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-008-016-4
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LENGTH: 458
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LOCATION: (1) - (1)
COTHER INFORMATION: synthesized protein will have a formylmethionine residue at this
OTHER INFORMATION: position
                                                                                                                                                                1835 TDSTA------PDALDAQ-GLYQGVQCYNGYGPTENGVMSTIYPIDSTE 1876
LYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYP--SETRMAHMATIAFDGASYEIYSALL 1774
                                                                           1775 FGRTLVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVV 1834
                                                                                                                                                                                                                                                 1877 SFI----NGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDKA-LDENRF 1932
                                                                                                                                                                                                                                                                                                                               1933 VHITVNDQTV---KAYRIGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRD 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                              500 VSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASML 559
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                       378 AVLKAGAAYVPLDAAYPADRIAYTVGDAGLAVVVTTSADFPDVD---GVRLLAPESLAE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Farnet, Chris
APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                 1990 SSVRDA---AVVLQQ---NEDQAPEILGFVVADHDHS 2020
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Patent No. US20020164747A1
GENERAL INFORMATION:
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Db 372 QDDGTLVGGKLEGADNDCLNDYQKF-KDQPAGVIVGPDSRPTLSFTSGSEGIPK 424	QY 650 GIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCVCIP 705	QY 706 SDDDRANSIPSFINRYNVNWAMATPSYMGTFSPEDVPGLATLVLVGEQMSSS 757 :	OY 758VNAIWA-PKLQLLNGYGQSESSSICFASNMSTEPNNMGRAVGAHS 801     :   :	Qy 802 -WVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWY 851   1   1   1   1   1   1   1   1   1	Qy 852 -PANTFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAI 899     ::  :  :    :	Qy 900 ETHLRQQMPDDLIIVVEATKRSQSANSTSLIAFLIGSSYFGNRPSDA 946	OY 947 HILDHDATKAINIKLEQVLPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDIL 1001	QY         1002         DKQTQGAIVQQAPAPIPVFADTAA	Qy 1038 DPATVNVGATFFELGGNSITAIKMVNMARSVGMDLKVSNIYQHPTLAGISAVVKGD 1093 	PLSYTLIPKSTHEGPVEQSYSQGRLMFLDQLD   :	1126 VGSLWYLIPYAVRMRGPVN     :       969 SGSVNVFVTGATGFLGSF1	Oy 1171 GVGVQIVHEKLSEBMKVI 1188 	RESULT 15 US-09-738-626-6480 ; Sequence 6480, Application US/09738626	zĸz		CANT	; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ; FILE REFERENCE: 249-125 ; CURRENT APPLICATION NUMBER: US/09/738,626 ; CURRENT FILING DATE: 2000-12-18 ; PRIOR APPLICATION NUMBER: JP 99/377484 ; PRIOR FILING DATE: 1999-12-16
QY 1790 ARALKDVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTD 1836 THE STATE ST	FINGVPIGRALNNSGAYVV 	DPEQQLVGIGVMGELVVTG-DGLARGYSDK-ALDENRFVHITVNDQTVKAYRTG		SULT 14		APPLICANT: Bhattacharyee, J. ; APPLICANT: Suvarna, Kalavati; APPLICANT: Bhattacheryee, Vasker ; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN	; Title Reference: 96.247-A . ; CURRENT APPLICATION NUMBER: US/09/994,595 ; CURRENT FILING DATE: 2001-11-27	LAILON NUMBER: 00/030,009 WG DATE: 1997-05-20 SEQ ID NOS: 160 Algrosoft Word 97	; SEQ ID NO 8 ; LENTH: 1391 ; TYPE: PRT ; ORGANISM: Candida albicans	Query Match  2.7%; Score 434.5; DB 9; Length 1391;  Best Local Similarity 19.8%; Pred. No. 2.5e-22;  Matches 229; Conservative 206; Mismatches 402; Indels 321; Gaps 49;	OY 233 THFWQTHLNDLNASVFPHLSDHLMVPNPTTTAEHRITFPLSOKALSNSAICRTALSI 289	QY 290 LLSRYTHSDEALFGAVTEQSLPFDKHYLADGTYQTVAPLRYHCQSNLRASDVMDAIS-SY 348	OY 349 DDRLGHLAPFGLRDIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPC 408 ::::::::::::::::::::::::::::::::::::	QY 409 NNRALLHCQMESSGALLVAXYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSS 462  Db 149 TVEGSIRDLAIYTDGTKFTIXYNALLYSHERVVICGEQFAQLTTVSGDTD 198	OY 463MAEVNLMTEYDRAEIESWNSQPLEYQDTLIHHEMLKAVSHSP 504	QY 505 TKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKS 564 1  :::   ::   ::    : 59 SKTRNFSYHKLIKLLIVVGNYLKETGIK-KGDIVMIXAYRGVDLMIAVMGVLKA 311	QY 565 GNAFTLIDPNDPPARTAQVVTQTRATVALTSKLHR 599      ::

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955 KAINIKLEQVLPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAP 1014
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                                                                                                                                                                                                                                                                                                                                                                              495 EMLKAVSHS-PTKTALQAWDGD-WTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSK 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 ISVVSTVPTLAGLWPAEALSQVRLLIVGGEACSQELVERLSTPDREVWNTYGPTEATVVA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    723 VNWMMATPSYMGTFSPEDVPGLATLVLVGEQMSSS-VNAIWAPKLQLLNGYGQSESSSI- 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 DDELLQSVSASDDFSSLTKSQDLAYVIFTSGSTGDPKGIMIEHR-----AFSSCALKF 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 HPSGPLGPEDRVLAGLSVAFDASCEEMWLAWGHGACL-VPAPRSLVRSGMDLGPWLIRRD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       841 SPFFTDIPSWYPANTFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIE 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----THLRQQMPDDLTIVVEATKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDAT 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 ANVAALSNVRSS-----AVVVQTT----GADQKVLVAYV-----SLEDAAAGFDHNVA 454
                                                                                                                                                                                                                                                                                                                                                                                                         ::|::|::| | | | | | | | :|| : | | : |:|
DVLESVASTYPEAAAID--DGQVLTYAELMEEVTALADSIHAQGIRRGDRIGIRMPSGTR 81
                                                                                                                                                                                                                                                                                                                                  Conservative 112; Mismatches 243; Indels 102;
                                                                                                                                                                                                                                                                                   2.6%; Score 424; DB 9; Length 1295; 25.8%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 00/159162
FILING DATE: 2000-04-07
                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1068 VGMDLKVSNIYQHPTL 1083
                                         PRIOR APPLICATION NUMBER: JP 00, PRIOR FILING DATE: 2000-08-03, NUMBER OF SEQ ID NOS: 7059; SCYTWARE: Patentin ver. 3.0 LENGTH: 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::| || |
549 KVPTAAVRDLYDHPRL 564
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Best Local Similarity
Matches 159; Conserv
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Search completed: May 30, 2003, 13:01:36 Job time : 105 secs



5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2003

OM protein - protein search, using sw model

Run on:

May 30, 2003, 12:33:51 ; Search time 39 Seconds (without alignments) 3327.678 Million cell updates/sec

US-09-482-788-2 16128 1 MEYLTAVDGRQDLPPTPASF......RVEHLLEEVSKTFEGLNSSL 3129 Title: Perfect score: Sequence:

112892 segs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	۵	Q 800	q 900	408 P	P39847 bacillus su	147	ра	Δ	ğ		P27206 bacillus su					⊣			bacil	bacil	Q08787 bacillus su					Ð	P40976 schizosacch	P07702 saccharomyc	Q01757 streptomyce	vibrio	57	P39581 bacillus su	35
SUMMARIES	ΙD	TYCC_BACBR	BACC_BACLI	BACA_BACLI	TYCB_BACBR	PPS3_BACSU	SRF2_BACSU	PPS2_BACSU	GRSB_BACBR	BACB_BACLI	HTS1_COCCA	- 1	- 1				ACVT_PENCH	ACVS_PENCH	SID2_USTMA		PKSK_BACSU		GRSA_BACBR	TYCA_BACBR	HMP2_YEREN		ENTF_ECOLI	LYS2_SCHPO	LYS2_YEAST	ACVS_STRCL	ANGR_VIBAN	LYS2_CANAL	DLTA_BACSU	DLTA_LACCA
	Length DB	486	359	255	587	2555 1	587	260	451	209	217	587	561	712	649	770	791	746	947	278		274	860		035	293		419						506 1
æ	Query Match 1	2	ς.	÷.	Ξ.	11.2	;	Η.		。	。					•	•	•	•		•		•		•	•		•				•		2.4
	Score	œ	1975	1882.5	1816	1807.5	1793.5	1769.5	1758	1710	1625.5	1613	1604	1515	1484.5	1422.5	1347.5	1346.5	928	909.2	852	756	742	740	654.5	268	559	514	494.5	469	451	434.5	408.5	383
	Result No.	1	7	ო	4	2	9	7	ω.	σ	10	11	12	13	14	15	16	17	18	13	20	21	. 22	23	24	25	56	27	28	29	30	31	32	33

P38135 escherichia	P40806 bacillus su 094049 candida alb	P17814 oryza sativ	P31119 escherichia	P08659 photinus py	Q9s725 arabidopsis	O24146 nicotiana t	P41636 pinus taeda	Q42524 arabidopsis	.027549 cryptospori	-	
YDID_ECOLI	ACSA_CANAL	4CL1_ORYSA	AAS_ECOLI	LUCI_PHOPY	4CL2_ARATH	4CL2_TOBAC	4CL_PINTA	4CL1_ARATH	ACSA_CRYPV	4CL2_PETCR	
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548	675	563	V 1.5	220	226	542	537	561	694	544	
1.7	1.5	1.5	ς; ,	T . 4	1.4	1.4	1.4	1.4	1.4	1.4	
280	244.3	242	235.5	233.5	230.5	228.5	226	225	222.5	221	
34	36	37	20 cm	3,5	40	41	42	43	44	45	

## ALIGNMENTS

381 TSYDLNVVVALAPSNELYVKLSYNAAVYESSFVNRIEGHLRTVI 424	455 QSPLDLSSMAEVNLMTEYDRAE-IESWNSQPLEV-QDTLIHHEMLKAVSHSPTKTAIQ 510 ; ; ; ; ;     ;   ;   ;   ;   1;   3.0 interpolation of the contraction of th	AWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTL	485 CGEDTLTYQELMERSAQLANALREKGI-ASGSIVSIMAEHSLELIVAIMAVLRSGAAYLP 543 571 IDPNDPPARTAQVYTQTRATVALTSKLHRETVOKLVGRCVVVDDELLOSVSASDDFSSLT 630		631 KSQDLAYVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGA 687	AF DOLOGIET I 1000010NF NORMILINGOLVI I I MWANNY I VQOB AYDF FILODOLOF DE 111 THE MANNY I VQOB AYDF FILODOLOF BET	688 CLLEIMTTLINGGCVCIPSDDDRMNSIPSFINRINVNMMATPSYMGTFSPEDVPGLATL 747 :       :	748 VLVGEQMSSSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRA 796 :	797 VGAHSWUIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPA 853	854 NTFPDGAKLYRTGDLARYASDGSIVCLGRIDSOVKIRGORVELGAIETHLRO-OMPDDLT 912 	913 IVVEATKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKA-INIKLEQVLPRHSIP 971 :     :     :     1   1   1   1   1	972 SFYICMLELPRTATGKIDRRRLRIMGKDILDKGTOGAIVQQAPAPIPVFADTAAKLHSIW 1031 	1032 VQSLGIDPATVNVGATFFELGGNSITAIKMY-NMARSVGMDLKVSNIYQHPTLAGISAVV 1090           :   :       :       : : : : :	1091 -KGDPLSYTLI-PKSTHB-GPVEQSYSQCRLWFLDQLDVGSLWYLIPYAVRMRGPVNVDA 1147 	1148 LRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTT 1207 	1208 PFNLSSEAGWRATLLRLGEDDHILTIVWHHIISDGWSIDVLRRDLNQLYSAALKDSKDPL 1267	1268 SALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSP-AKIPTDFARPALLSGDA 1324 	1325 GCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPE 1384 	1385 LEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGSRDL 1444 	1445 SSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTRFDMEFHLFQETDSLKG 1498   1
qq	Qy Db	Oy	qa ò	g q	\$ 6	3 8	oy Op	oy da	Qy	Oy Dp	. VQ	Oy Db	oy do	Qy Dp	Qy	Qy	Qy	Oy Dp	QY Db	Qy
CC or send an email to license@isb-sib.ch).	DR EMBL; AF004835; AAC45930.1; DR HSSP; P14687; IAMU. DR InterPro; IPR000873; AMP-bind.	InterPro; IPR001242; Condensatn. InterPro; IPR003880; Ppantne_att InterPro; IPR000379; Ser_estrs_s	DR InterPro; IPROULO31; Thioesterase. DR Pfam; PF00550; pp-binding; 6. DR Pfam; PF00550; pp-binding; 6.	Pfam; PF00668; Pfam; PF00975; PRINTS: DR00154	PROSITE; PS00012 PROSITE; PS00455 PROSITE: PS50075	Ligase: Artibiotic migrations Multifunctional engage	NW MULLILUICCIONAL ENZYME; REPEAT.  FT REPEAT 466 1038 DOMAIN 1 (ASPARAGINE-ACTIVATING). FT REPEAT 1521 2070 DOMAIN 2 (GLUTAMINE-ACTIVATING). FT REPEAT 5536 3113 DOMAIN 3 CONDELACTIVATING).	REPEAT 2530 5113 DOMAIN 3 REPEAT 4606 5203 DOMAIN 4 REPEAT 5658 6245 DOMAIN 6	DOMAIN         970         1037         ACYL CARRIER           DOMAIN         2007         2074         ACYL CARRIER           DOMAIN         3045         3112         ACYL CARRIER           DOMAIN         4080         4147         ACYL CARRIER	DOMAIN   5124   5191   ACYL CARRIER (ACP) 5.	410 4110 PHOSPHOPANTETHEINE (B 4110 4110 PHOSPHOPANTETHEINE (B 5154 5154 PHOSPHOPANTETHEINE (B 6197 6197 PHOSPHOPANTETHEINE (B	b 12.9%; Scor Similarity 23.0%; Pred 64: Conservative 595; M	46 IEAIKPCTPFQLDMIDCNALDKQSAIGHAVXDVPTDIDISRFALAWK	93 EIVNQTPALRAFARTSDSGKTSQVILKDSFVFSWMCWSSSSSPDEVVRDEAAAAASGPRC	153 NRFVLLEDMQTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPE 1	204 TPESSDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLNDLNASVFPH		311 P-FDKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISXDDRLGHLAPFGLRD	INTERPRETATION TO THE TRANSPORT OF THE T	407

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11. PATHWAY: CYCLIC peptide antibiotic bacitracin biosynthesis.
12. SIBUNIT: LARGE MULTIERZYME COMPLEX OF BAI, BA2 AND BA3.
13. SIBUNIT: LARGE MULTIERZYME COMPLEX OF BAI, BA2 AND BA3.
14. SOBUNIT: LARGE MULTIERZYME COMPLEX OF BAI, BA2 AND BA3.
15. 1- DOMAIN: CONSISTS OF FIVE MODDLES, AND A DUTATIVE C-TERMINAL
15. THE DESTINERASE DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO
16. THE DESTINE FROUGT AND CAN BE FUGTHER SUBDIVIDED INTO DOMAINS.
17. RESPONSIBLE FOR SUBSTRATE AND CAN EPIMERIZATION (OPTIONAL).
17. METATION (OPTIONAL).
18. MISCELLANBOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC
19. MISCELLANBOUS: BACITRACIN A, BRANCHED CYCLIC DODECAPEPTIDE: IT
17. CONTAINS AN N-TERMINAL LINEAR PENTAPEPTIDE MOIETY (ILE-CYS-LEU-D-
17. GLU-ILE) WITH AN ISOLEUCINE-CYSTEINE THIAZOLINE CONDENSATION
17. CONTAINS FOUR FIRE FREE ALPHA-CARBOXY GROUP OF THE C-
18. TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE: IT
18. DECOMPANINS FOUR AMINO ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANINS AND AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANINS AND AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANINS AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7), DECOMPANING FOUR AND ACIDS IN THE D-CONFIGURATION (GLU-4, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
Bacitracin synthetase 3 (BA3) [Includes: ATP-dependent isoleucine
adenylase (IneA) (Isoleucine activase); ATP-dependent D-phenylalanine
adenylase (D-PheA) (D-phenylalanine activase); ATP-dependent histidine
adenylase (D-SAPA) (Histidine activase); ATP-dependent histidine
adenylase (D-AspA) (C-aspartate activase); ATP-dependent asparagine
adenylase (BC 5.1.13); Phenylalanine activase); ASPATtate racemase
(EC 5.1.13); Phenylalanine racemase [ATP hydrolyzing]
BACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: L-aspartate = D-aspartate.
-i- CATALYTIC ACTIVITY: ATP + L-phenylalanine = AMP + diphosphate + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. Biol. 4'927-937(1997).
-i- FUNCTION: INDUCES PEPTIDE SYNTHESIS, ACTIVATES AND INCORPORATES
FIVE AMINO ACIDS, FORMS A THIAZOLINE RING BETWEEN THE FIRST TWO
AMINO ACIDS AND INCOPORATES A D-GLUTAMINE IN THE FOURTH POSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Konz D., Klens A., Schoergendorfer K., Marahiel M.A.;
"The bacitracin biosynthesis operon of Bacillus licheniformis ATCC
10716: molecular characterization of three multi-modular peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: CONTAINS 5 COVALENTLY BOUND PHOSPHOPANTETHEINES (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Firmicutes; Bacillales; Bacillaceae; Bacillus
3491 GNAKFDLTL--EAHEDETGIHFALVYSTKLFORESIERM 3527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: CONTAINS 5 ACYL CARRIER DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98089193; PubMed=9427658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF007865; AAC06348.1; -. HSSP; P14687; 1AMU.
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHE-9, AND ASP-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-ATCC 10716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phenylalanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetases."
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                                                                                                                                               BACC_BACLI
                                                                                                                  RESULT 2
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60. ELLRA-SFHHRLDEPLHVIKDRHMKFDYLDIRGRHDQDGVLERYLAE----DRQKGFDL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESS-----HEMPCNNRALLL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALRAFAFTSDSGKTSQVILKDSFV-FSWMCWSSSSSPDEVVRDEAAAAASGPRCNRFVL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AKDTLMRACLIRMSDDSYQFVWTYHHILLDGWCLGIILDELLTIYEMKRKGONHQLEDPR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 PETPESSDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLNDLNASVFPHLSDHLMVPNPT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 ELKN--DLIDHVMVFENYAVDQKAFEEKNDV-GF-EMVNVSGEEQTNYHF----- 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCQMESSGAL----LVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPL--DLSSMAEVNL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SISAALDDQLKLLFIYDENVYD---TTIIETLEKHIITVAEQVAEDETQTLRDINL 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSLPFDKHYLADGTYQTVAPLRVHCQSNLRASDVM-----DAISSYDDRLGHLAPF-GLR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQ 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKVEKIYPLSNMQKGMLFHAMKDEAS---HAYFEQFIIELKGDVDERMFEESLNEVMKRH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERRREKTIECS-KELTNRLIKLANRNHVTINTVLQSIWGVILAKYNNSEDVVFGTVVSG
                                                                                                                                                                                                                                              DOMAIN 2 (D-PHENTLALANINE-ACTIVATING).
DOMAIN 3 (HISTIDINE-ACTIVATING).
DOMAIN 4 (D-ASPARTIC ACID-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 SRIEAIKPCTPFQLDMIDCNALDKQSAIGHA·····VYDVPTDIDISRFALAWKEIVNQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEDMQTKKC------QLVWTFSHALVDVTFQQRVLSRVFAAYK------HEKDTHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYSDYIKWLEDQDKE------EAQSYWESYLSGYDQK---NSLPKLRTPSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 TTAEHRITFPLSQKALSN-----SAICRTALSILLSRYTHSDEALFGAVTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDAEVEGIETMVGVFINTIPTRIRLDKDKLFKDVLRQTQADALESSRYNYMNLAEVQALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTEYDRAEI-ESWNSQPLEV-QDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSS
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461 1034 DOMAIN 1 (ISOLEUCINE-ACTIVATING).
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            InterPro; IPR001241; Condensatr.
InterPro; IPR001241; Condensatr.
InterPro; IPR001801; Thioesterase.
Pfam; PF00501; AMP-binding; 5.
Pfam; PF00550; pp-binding; 5.
Pfam; PF00550; pp-binding; 5.
Pfam; PF0051; Phioesterase; 1.
PRINTS; PR00154; AMPBINDING.
PROSITE; PS00012; PHOSPHOPANNETHEINE; 4.
PROSITE; PS000455; AMP_BINDING; 5.
PROSITE; PS00055; AP_DOMAIN; 5.
Ligase; Isomerase; Hydrolase; Antibiotic biosynthesis;
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å	THE DAMENT TO CALL TITLE TO THE TABLE TO THE	Qy 1621	1 PRSCETIVAFFGVLKANLAYLPLDVRSI
g qa		Db 1554	4 DRSPEMIIGLLGILKAGGAYLPLDPAY
ò	SGSTGDPKGIMIEHBAESSCALKEGASLGINSDTBALOFGTHAEGACLLEIMTTLINGG	Qy 1681	1 VEFVRIRDALNDSNADGFEVIEHDSTK
. A		Db 1607	7 RAFIKEADMINIDIHDK-QIAAQDAAQI
۸٥	VCIPSDDDRMNSIPSFINRYNVNWMMATPSYMCTFSPEDVPGLATLVLVGEOMS-	Qy 1737	
qa	AEVIKKEQVSVMFITTALFNTLADINIGCLAKLRKIFLGGERASI	Db 1666	6 SNLVSAVVKLMHLNTGSRVIQFASLSFI
Οy	756SSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNNGRAVGAHSWVID 805	Qy 1796	
qa	:  ::   ::  :  :    :    :   :    :  :	Db 1726	6 -FLRQYNITHATLPPTVLDVI
δλ	806 PNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANT 855		6 -NGYGPTENGVMST-~IYPIDSTESFII
qa	EELTAE		1778 INAYGPTETTVCATAGIYEG
. Оу	856 FPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGALETHLRQQMPDDLTI 913		1912 VVTGDGLARGYSDK-ALDENRFV-HITT
QQ	825 FIPGERLYKTGDLAKWLPDGNIEFIGRIDHQVKIRGFRIELGEIESRLEMHEDINETI 882	•	1031 CVGGGSLARGI LNRFELLAENFLSHFF
οy	914 VVEATKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSF 973		O FKIRGNRIESAEIEAALLRDSSVRDAA
qq		DD 1886	1888 VKIRGYRIELGEIENQLLKLDKIDEAA
Oy	974 YICMLELPRTATGKIDRRELRIMGKDILDKQTQGAIVQ-QAPAPIPVFADTAAKLHSIWV 1032	Qy 2030	0 QVEGWQDHFESGMYSDIGEIDPSTIGS
- qq		. Db 1937	1
Ċ	1033 ACK TINDBAUNUCAPPET CONTRATANTAN WATANT NOT A THOUSAND TO SEE THE SECOND S	Oy 209(	2090 RSLGNVLEIGTGSGMILFNLDSRLESY
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00 i	3/0 DIENVERBGIN-THEFERGERBLAAAAMAAKIRREENABIFLGGIFRIFIIRGEGIIK 1033	Qy 2150	0 ATDIGOVDDLHPDLVVLNSVIQYF
ŠÕ i	GDFLS-TILLFKSTHEGEVEQSISGGRLWFLDQLDVGSLWILLPYAVRMRGPVNVDALRR	Db 1967	
gg	STKDSVYSSIQKVEEKEYYRLSSAQKRLYILDQIEGSGLSYNIPFTMKVKGRFDIRRFEN	Qy 2205	5 TNEHFLAARAIHTLGKNAT
Oy	1151 ALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEWKVIDLCGSDLDPFEVLNQEQTTPFN 1210		:       ISHHFFAAGGDSIK
qa	1094 ALKTIIQRHEALRTSFLMADGEPVQKIEKEVDFSIKCSKIQSLSIQEIIKQ-FVRPFD 1150	Ov 2255	S FPGLVEHVETLPKNMEAVNE
QY	1211 LSSEAGWRATLLRIGEDDHILTIVWHHIISDGWSIDVLRRDLNQLYSAALKDSKDPLSAL 1270		
qq	1151 LKKAPLERTEVVKVDDEEHILLFDMHHIISDGASMGVLTKEICDLYGGKEL 1201		TACTOR TOWN COUNTY TO STATE OF THE STATE OF
QY	1271 TPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSPA-KIPTDFARPALLSGDAGCV 1327		
qq	1202 KPLSLQYKDYSEWGRDFYQKDEMKRQKEYWLNIFKGEIPVLNMPTDYPRPQMHSVEGDRI 1261		ALKMIYEEKGGDFIQYNKSF
Qy	1328 HVIIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELED 1387		:   :   :   :   :   :   :   :   :   :
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Qy	1388 IIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGSRDLSST 1447		
qa	:	Db 2221	
Óy	1448 PLAQLIFAVHSOKDLGREKFQGLESVPVPSKAY-TRFDMEFHLFOETDSLKGSVNFADEL 1506	Qy 2457	7YMIPSNIVVLDKMPLNANGKVDRK: ::
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δλ	1507 FKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHVDYP 1560	Qy 2514	ATEVFG
qq			ATADL
Qy	1561 RESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAVFA 1620	Qy 2561	(1SVIRO) (1
. a	1494 TDKTICQLFAERAETSPDKTAVVFEDQTLTYRQLHERSNQLARFLREKGVQPDTAVGIMV 1553	Db 235	2359 DITRIIGWETTMYPVLLDAGEEKALSO

TVNDQTVKAYRIGDRVRYRIGDGLIEFGRMDTQ 1969 ::::||||| |::|| :|| ||| ||| PASGE--RLYRIGDLARW-LPDGHLEFLGRIDHQ 1887 KELSRRAKVVPKQQTAAPLPTFPISEVEVILCEE 2513 FDGASYEIVSALLEGRILVCVDYMTTLDARALKD 1795 || ::||: || || : : | |FDASAFEIFPALAAGSALVLGRQEEMMPGQPLTS 1725 VENESGLENLKVIVSAGSACSEELAKRWSGNRLF 1777 INGVP-IGRALNNSGAYVVDPEQQLVGIGVMGEL 1911 SGRPHIGSPIANTNVYVLDQNQKPVPTGVVGEL 1830 AVVLQQNEDQAPEILGFVVADHDHSENDKGQSAN 2029 ||: ::::| : ::|: | AVIARKDDHSDYLCAYIVSKED------ 1936 SDFKGWTSMYDGSQIDFDEMHEWLGETTRTLHDN 2089 YVGLEPSRSAAAFVNKATESIPSLAGKAKVQVGT 2149 FPSSEYLAEIADTLIHLPNVOR--IFFGDVRSOA 2204 | :: |:: | : | | APRINDITEAKLVD-----IWRDVLGAGDI---G 2016 TKDDVRQKMA--ELEDMEEELLVEPAFFTSLKDR 2254 ELSAYRYAAVVHVRGSLGDELVLP----VEKDD 2302 || : : |: :| : | : | : | ELDHFNQSFVLFRKGGFDESCVKKAFNKIMEQHD 2129 LLKSSDAAIMAVSKIPFEITAFERQV--VASLNS 2350 DSSLSVPDIFRIAGEAGFRVEVSSARQWSQNGAL 2400 LRGSDLLTNRPLQRLQNRRIAIEVRERLRSLLPS 2456 : | |: : | : : | : : | OEFA-----RRLKAYAHSRTLSKEAEYWRNIAKA 2275 | | | : : : | :| XENS------TTLSIKLGKE 2304 LATKLISRI----DQRLKVRIT---VKDVFD-- 2560 | | | | :: :||| : :||| : LLTALLTGARDITGENKLKVMMEGHGREDILEGV 2358 SPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTN 1680 RLSRTLMFFFLVVTDSTAPDALDAQGLYQGVQCY 1855 QGL----GLQQPVSDGQGQDRSAHMAPRTETEA 2601 

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 ILCDEFAKVLGFQVGITDNFFDLGGHSLMATKLAVRIGHRLDTTVSVK---DVFDHPVLF 2658
                                                                                                                                    2530 LEEIKG--KYRSAIEKIYPLANMOKGMLFHAIEDHTSDAYFQQTVMDIEGYVD-PAILEA 2586
                                                                                                                                                                                          SFNDIMKRHEIL------RASYE-YEIV----EEPRQIIIENRSIDFTYFNIAK 2629
                                                                                                                                                                                                                                           SSAQQQEMFIERLINEDRKKGFDLSKDVLMRAYLLKTAERSYRLVWSHHHILLDGWCLGI 2689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LTKF-----VNIEMDEPLYDLAIAGEVEPDGAGLKVTVIAKTQLFGRK--RVE 3112
                                                                                                                                                               2752 DAAGLIKACESLVNHLDIFRTVFAEASGELYQVVLSCLDLPIQVIETEDNI-----NTAT 2806
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                                                     -QLAIALDNLVQSKTNEIVGGREMAEYSPFQLLFTEDPEEFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
15-JUR-2002 (Rel. 41, Last annotation update)
Bacitracin synthetase 1 (BA1) [Includes: ATP-dependent isoleucine
adenylase (CIAA) (Isoleucine activase); ATP-dependent cysteine
adenylase (CYAA) (Cysteine activase); ATP-dependent leucine adenylase
(LeuA) (Leucine activase); ATP-dependent glutamate adenylase (GluA)
(Soleucine activase); ATP-dependent isoleucine adenylase (ILAA)
(Isoleucine activase); Glutamate racemase (EC 5.1.1.3)].
                          2416 FTNEEKARISFNYLGDIDADMNRGEFSGSSFSEGESIGGKIARSHSIEINAIVMNHELVI
                                                                               2476 HTTFNOMEYEKDTISRLNHOLKERLEQIIKHCTQQTESERTPSDYGDTNISLAE----
                                                                                                           ----DHTT----ARPRPFVPFYIDFPSTSEP
                                                                                                                                                                                                                   NE-----FLDEFAKEPVRLGHPLIRFTIIK-----QTKSMRVIMRISHALYDGLSLEH
                                                                                                                                                                                                                                                                         VVRKLHMLY - - - - NGRS - - LLPPHQFSRYMQY - TADGRESGHGFWRDVI - - - - QNTPMTI
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                                                                                                                                                                                                                                                                                                                              LSDDTVVDGNDATCKALHLSKIVNIPSQVLRGSSNIITQATVFNAACALVLSRESDSKDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                       --ETIGFSDLKRNCTDWPEAITNFSCCITYHNFEYHPESQFEQQRVEMGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The bacitracin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecular characterization of three multi-modular peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n. Biol. 4:927-937(1997).
FUNCTION: ACTIVATES FIVE AMINO ACIDS, INCORPORATES TWO D-AMINO
ACIDS, RELEASES AND CYCLIZES THE MATURE BACITRACIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillales; Bacillaceae; Bacillus.
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STRAIN-ATCC 10716;
MEDLINE-98089193; PubMed-9427658;
"Yang A., Schoergendorfer K., P
                                                                                                          2700 ASEIKPQLELQEIIQDIYPSTQMQKAFLF-
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"The bacitracin biosynthesis operon
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                                                                                                                                                                                                                                                                                                     (OPTIONAL), AND
                                                                                                                                                                                                                                                     RESPONDIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL). AND METHYLATION (OPTIONAL). AND EPIMERIZATION (OPTIONAL). AND METHYLATION (OPTIONAL). AND METHYLATION (OPTIONAL). AND METHYLATION (OPTIONAL). AND METHYLATION (OPTIONAL). THE MOST DODECAPEPTIDES. THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST CONTAINS AN N-TERMINAL LINRAR PENTAPEPTIDE MOST (ILE-CYS-LEU-D-GLU-ILE) WITH AN ISOLEUCINE-CYSTEINE THIAZOLINE CONDENSATION PRODUCT AND A C-TERMINAL HEPTAPEPTIDE RING (LYS-D-ORN-ILE-D-PHE-HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE C-TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDSSRIEAIKPCTPFQLDMIDCNALDKQSAIGHAVYDVPT-----DIDISRFALAWKEI
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                                                                                      PATHWAY: Cyclic peptide antibiotic bacitracin biosynthesis.
SUBUNIT: LARGE WULTIENZYME COMPLEX OF BAI, BA2 AND BA3.
DOMAIN: CONSISTS OF FIVE MODULES AND ONE EPIMERIZATION DOMAIN I
THE FOURTH MODULE. EACH MODULE INCORPORATES ONE AMINO ALID INTO
THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
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PHOSPHOPANTETHEINE (BY SIMILARITY)
PHOSPHOPANTETHEINE (BY SIMILARITY)
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PROSITE; PS00455; AMP BINDING; 5.
PROSITE: PS00405; ACP_DOMAIN; 5.
Ligase; Isomerase; Attibiotic biosynthesis; Phosphopantetheine; Multifunctional enzyme; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOPANTETHEINE (BY SIMILARITY)
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DOMAIN 3 (LEUGINE-ACTIVATING).
DOMAIN 4 (GLUTAMINE-ACTIVATING).
DOMAIN 5 (ISOLEUCINE-ACTIVATING).
CYCLIZATION (POTENTIAL).
                           CONTAINS 5 COVALENTLY BOUND PHOSPHOPANTETHEINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN 1 (ISOLEUCINE-ACTIVATING)
DOMAIN 2 (CYSTEINE-ACTIVATING).
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ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 4.
ACYL CARRIER (ACP) 5.
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CATALYTIC ACTIVITY: L-glutamate - D-glutamate.
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%; Pred. No. 3.6e-100;
603; Mismatches 1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 5 ACYL CARRIER DOMAINS.
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Interpro: IPR001242; Condensatn.
Interpro: IPR001880; Ppantine_attach.
Pfam: PF00501; AMP-binding; 5.
Pfam: PF00550; Pp-binding; 5.
Pfam: PF00668; Condensation; 5.
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                                                                 (POTENTIAL)
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Best Local Simil
Matches 777; C
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Db 2693 CFYIDRKTEEKPYYRLSSAQKRLYILSQTGSHVAYNMPFAMTLEGDFDIRRFENTL 27	QY 1153 AALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLGGSDLDPFEVLNOEQTTPFNLS 1212  : :	QY 1213 SEAGWRATLIRIGEDDHILTIVMHHIISDGWSIDVLRRDLWQLYSAALKDSKDPLSALTP 1272	OY 1273 LPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSPA-KIPTDFARPALLSGDAGCVHV 1329	QY 1330 TIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDII 1389	QY 1390 GCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPPERVVSALQPGSRDLSSTPL 1449  1           :     :       :	QY 1450 AQLIFAVHSQKDLGRFKFQGLESVPVPSK-AYTRFDMEFHLFQETDSLKGSVNFADELFK 1508 1036 FDTMLVYHN-TDVKPFFABGLRSRLVEIKRGISKFDITVTASEAADGLRLEVEYSTTLFN 3094	QY 1509 METVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVL-NVKHVDYPRESSL 1565    :  :  :  :  :  :  :  :  :  :  :  :  :	QY 1566 ADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAVFAPRSCE 1625 :: :	QY 1626 TIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVR 1685	OY 1686 IRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTS 1742	QY 1743 GCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALKDVFFREHV 1802  1323 RIYQHLDAHLNVALVAPYIFDASVKQIFAALLFGHTLCIVPRETAMDAMSLIEYYSKNNI 3382	QY 1803 NAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDAQGLYQGVQC- 1854	QY 1855 -YNGYGFTENGVMSTIYPIDSTESPINGVPIGRALNNSGAYVDPEQQLVGIGVM 1908	QY 1909 GELVVTGDGLARGYSDK-ALDENRFVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMD 1967	QY - 1968 TQFKIRCNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAFEILGFVVADHDHSENDKGS 2027   1   1   1   1   1   1   1   1   1	QY 2028 ANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLH 2087	QY         2088 DNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEPSRSAAAFVNKATESIPSLAGKAKVQV 2147           Db         1   1   1   1   1   1   1   1   1   1	QY 2148 GTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRIFF 2197
95 VNQTPALRAFATSDSGKTSQVILKD-SFVFSWWCWSSSSSPDEVVRDEAAAAASGPRCN 153 :	EQQRVLSRVFAAYKHEKDTH	RPETPESSDATDTDSQSVSVSMSCEDNAVSATHFWQTHLNDLNASV-FPH	AEHRITFPLSQKALSNSAICRTALSILLSR  :  :  :  :  :    :	VHCQSNLRASDVMDAIS :: :   : NEVDTSYSFKEFLQQTKERTIA	347 SYDDRLGHLAPFGLRDIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFL 396   :-	HLIK ::: 'RILE	HEMLKAVSHSPTKTAIQ       : QLFEEQAKRIPDHTAVV	511 AWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTL 570 1			SPED :   TALD		TEPD       		TKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICM	LELPRTATGKIDRRRLRIMGKDI-LDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLG	1037 IDPATVNVGATFFELGGNSITAIKMYN-MARSVGMDLKVSNIYQHPTLAGISAV-VKGDP 1094	I SVTI. I DKETHPC DVPO. SVEOCE I III I OCI INCE - I INVI TRVAVI I INVINITATI I INVINITATI I INVINITATI I INVI

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 --PPRNEIERKLVQVWREILGAEDIGISHHFFAAGGDSIKALQIVSRL--
                                                                     AKMNLKLEMKALFANPKIKDLSRFITEETRHRKHNKPVTGETELLPIQKRYFANNKEELD
                                                                                                                                                                                                                                                     2376 FRIAGEAGFRVEVSSAROWSONGALDAVFHHCCSOGRTLVNFPTDHHLRGSDLLTNRPLQ
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                                     GDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELL-VEPAFFTSLKDRFP
                                                                                                          GLVEHVEILPKNMEAVNEL-SAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKS
                                                                                                                                            HFNQSFMLFRKDGYDENIVRTAFNKILEQH-----DALRMIYEEKDGDIIQYNRGYREN
                                                                                                                                                                                 LGDLLKSSDAAIMAVSKIPFEITAFERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDI
                                                                                                                                                                                                                   LFDL----DV-----YDVRGFDSQ------EEKVFELATGIQKKSSI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS
RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION
(NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND
MISCELLANGOUS: TYROCIDINE IS A MIXTURE OF FOUR CYCLIC
DECARPEPTIDES, TYROCIDINE A (D-PHE-PRO-PHE-D-PHE-ASN-GLN-TYR-VAL-
ORNN-LEU), B, C, AND D, IN WHICH PHE, AT POSITIONS 3, 4, AND TYR
RESIDUES ARE GRADUALLY REPLACED BY TRP, DEPENDING ON THE RELATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internal adenylation domains.";
J. Bacteriol. 179:6843-6850(1997).
-!- FUNCTION: ACTIVATES THE SECOND TO FOURTH AMINO ACIDS IN TYROCIDINE (IN TYROCIDINE A, PRO, PHE, AND D-PHE) AND EPIMERIZES THE LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Cyclic peptide antibiotic tyrocidine biosynthesis.
SUBUNT: LARGE MULTENZYME COMPLEX OF TYCA, TYCB AND TYCC.
DOMAIN: CONSISTS OF THREE MODULES, INCLUDING AN C-TERMINAL
EPIMERIZATION DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ∆
+
                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annother update)
15-JUN-2002 (Rel. 41, Last annother update)
15-JUN-2004 (Rel. 41, Last annother update)
Tyrocidine synthetae II [Includes: ATP-dependent proline adenylase (ProA) (Proline activase); ATP-dependent phenylalanine adenylase adenylase (D-PheA) (D-Phenylalanine activase); Phenylalanine racemase [ATP-hydrolyzing] (EC 5.1.1.11)].
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 8185;
MEDLINE=98012987; Pubmed=9352938;
MODCI H.D., Marahiel M.A.;
Mocta H.D., Marahiel M.A.;
The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequence and biochemical characterization of functional
                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + L-phenylalanine - AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: CONTAINS 3 COVALENTLY BOUND PHOSPHOPANTETHEINES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONCENTRATIONS OF THESE AMINO ACIDS IN THE GROWTH MEDIUM. SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PRO015; PHOSPHOPANTETHEINE; 3.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
PROSITE; PS00045; ARP_BINDING; 3.
PROSITE; PS50075; ACP_DOMAIN; 3.
Ligase; Isomerase; Antibiotic biosynthesis; Phosphopantetheine; Multifunctional enzyme; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 3 ACYL CARRIER DOMAINS.
                                             A.
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InterPro; IPR001242; Condensatn.
InterPro; IPR003880; Ppantne_attach.
Pfam; PF00501; AMP-binding; 3.
                                          PRT;
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Pfam; PF00668; Condensation;
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phenylalanine.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                  Bacillus brevis.
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                                      TYCB_BACBR
030408;
                    TYCB_BACBR
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britan K.D., Errinington J., Fabret C., Ferrari E., Fouger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghiseppi G., Guy B.J., Hagaa K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Murita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Wurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Monon D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadae Y.,
Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
RA Takeuchi M., Tamakoshi A., Taramakoshi H., Takamaru K.,
RA Takauchi M., Tamakoshi A., Taramakoshi A., Wanbutt R., Wadler E., Vassarotti A.,
R. Tosato V., Uchiyawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
R. The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A putative new peptide synthase operon in Bacillus subtilis: partial characterization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pognoni A., Franchi E., Magistrelli C., Colombo E., Cosmina P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiology 141:645-648(1995).
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R KSEP; 14687; 1AMU.
R SUDITISE; BG10972; ppsc.
R InterPro; IPR001897; AMP-bind.
R InterPro; IPR001897; AMP-bind.
R InterPro; IPR001890; Ppattne_attach.
R Ffam; PF00501; AMP-binding; 2.
R Pfam; PF00508; pp-binding; 2.
R PRNTS; PR00144; AMPBINDING; 2.
R PROSITE; PS00102; PHOSPHOPANTETHEINE; 1.
R PROSITE; PS00455; AMP_BINDING; 2.
R PROSITE; PS0075; ACP_DOMAIN; 2.
R MILLIGURCIONAL CARRIER (ACP) 1.
R DOMAIN 2008 2074 ACYL CARRIER (ACP) 2.
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11.2%; Score 1807.5; DB 1; Length 2555; 24.7%; Pred. No. 2.4e-96; ive 510; Mismatches 1114; Indels 457;

Conservative 510;

Similarity

Query Match Best Local Simi Matches 681;

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974 YICMLELPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQ 1033
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                                                                       .04 FAFTSDSGKTSQVILKDSFV----FSWMCWSSSSSPDEVVRDEAAAASGPRCNRFVL 157
                                                                                                         67 AFIYKNVAKPROVVLKORHCPIHIEDISHLNERDKEHCTEAFKEQ------DKSKGFDL 119
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1034 SIGIDPATVNVGATFFELGGNSITAIKMVN-MARSVGMDLKVSNIYQHPTLAGISAVVK- 1091	1208	1369 EDAVIGTPIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDI 1428	LEKLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGML  :	1666 LIGHDTAPPDIEUTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGR 1725  1	IRNVCPEVSIMOGYGENTERFESTCLHIOKTYELSIPIGRPVGNSTAFILNOWGYLOP  IGVWGELVYTGDGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDRYKYRIGDGLIE  IGVWGELVYTGDGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDRYKYRIGDGLIE  IGVWGELVYTGDGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDRYKYRIGDGLIE  IGVWGELVYTGDGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDRYKYRIGDGLIE  IGVWGELVYTGDGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDLARW-LSDGTIE  FFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQONEDQAPEILGFVVADHDHSE  IGVWGELCVGGGGVARGYLGREATALRDSSVRDAAVLARTAGTGSKELFGYISV  NDKGOSANQVE
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| : | | : | : : : : : : . | : : | - : | GQTIQLPPKTDSYQEY-ARRIQEYAQSSK 2272 ASLNSNIDEWQLSTIR-SSAEGDSSLSVP 2373 GRIAME --- GHGREHILPELDISRTVGWFT 2380 APLPTFPISEVEVILCÉEATEVFGMKVDIT 2525 OIMKHCAGQQKAEKTLSDFSSQSLTAEDLD 2546 SEELLVEPAFFTSLKDRFPGLVEH----- 2261 NARIAIEVRERLRSLLPSYMIPSN-IVVL 2466 PIKKGVGY-----GMLKYLTHPENKSITF 2433 | ::| | | SKDITHTWKREQII-----EMSAMAADKK 2487 cus responsible for surfactin DAVEHHCCSQGR-----ifA that contains the region Bacillus subtilis."; randi G., Perego M., ıza C., Nakano M.M., laceae; Bacillus ate) pdate) AA.

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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
R. Borriss R., Boursier L., Brans A., Braun M., Brigan I.S.C., Bron S.,
Borriss R., Boursier L., Brans A., Braun M., Brigall S.C., Bron S.,
R. Borrist S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
R. Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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R. Britz C., Fuljta M., Fuljta Y., Fuma S., Galizzi A., Galeron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
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A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
R. Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Joris B., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
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A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Persecan E., Puljt P., Purnelle B., Ropopott G., Rey M., Reynolds S.,
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The complete genome sequence of the Gram-positive bacterium Bacillus
F. Subtils F.,
Frit Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bronpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Borchert S., Patil S.S., Marahiel M.A.;
"Identification of putative multifunctional peptide synthetase gene:
using highly conserved oligonucleotide sequences derived from known
synthetases.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, ASP AND VAL. ACTIVATION SITES FOR THESE AA CONSIST OF IMPIVIDUAL DOMAINS.
-!- COFACTOR: CONTAINS SOVALENTLY BOUND PHOSPHOPANTETHEINES.
-!- PATHWAY: CYOLIC PEPTIGE ANTIBIOTIC SULFACELIN BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                             Yamane K., Kumano M., Kurita K.; "The 25 degrees 36 degrees region of the Bacillus subtilis chromosome: determination of the sequence of a 146 kb segment and identification of 113 genes."; Microbiology 142:3047-3056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 3 ACYL CARRIER DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetases.";
FEMS Microbiol. Lett. 71:175-180(1992).
                                                                                                                                                                                                             MEDLINE-98044033; PubMed-9384377;
                                                                MEDLINE=97124189; PubMed=8969502;
Mol. Microbiol. 8:821-831(1993)
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                                SEQUENCE FROM N.A.
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EMBL; D13262; BAA02523.1; -. EMBL; X70356; CAA49817.1; -.

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TVHQLFEETVQRHKDRPAVTY -> DGCISYSKRLSSATKT
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                                                                                                                                                   PRINTS; PR00154; AMPBINDING.
PROSTIE: PS00012; PHOSPHOPANTETHEINE; 3.
PROSTIE; PS00455; AMP_BINDING; 3.
PROSTIE; PS50075; AMP_BINDING; 3.
Ligase; Antibiotic biosynthesis; Phosphopantetheine; Sporulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.1%; Score 1793.5; DB 1; Length 3587; 22.4%; Pred. No. 2.8e-95;
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                                                                                                                                                                                                                                                         DOMAIN 2 (ASP-ACTIVATING).
DOMAIN 3 (D-LEU-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
PHOSPHOPANTETHEINE (POTENTIAL).
PHOSPHOPANTETHEINE (POTENTIAL).
PHOSPHOPANTETHEINE (POTENTIAL).
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D -> H (IN REF. 1).
GELCAA -> RAIRG (IN REF. 1).
RF -> L (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                               S -> G (IN REF. 1).
A -> G (IN REF. 1).
C -> D (IN REF. 1).
RQA -> AQG (IN REF. 1).
L -> W (IN REF. 1).
R -> A (IN REF. 1).
R -> A (IN REF. 1).
TPA -> SRP (IN REF. 1).
TPA -> SRP (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
RQSING (IN REF. 1).
RHV -> ETL (IN REF. 1).
RQSIT -> DKRIS (IN REF. 5).
M -> L (IN REF. 5).
                                                                                                                                                                                                                              Repeat; Complete proteome.
DOMAIN 1 (VAL-ACTIVATING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P -> R (IN REF. 1).
G -> E (IN REF. 1).
KRRADG -> E (IN REF. 1).
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R -> A (IN REF. 1).
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Matches 732; Conservative 458; Mismatches 1130;
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A -> V (IN REF. 1).
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F -> K (IN REF.
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H -> Q (IN R
V -> C (IN R
G -> V (IN R
                                           Subtilist; BG10169; srfAB.
InterPro; IPR001873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR03880; Ppantne_attach.
Fram; PF00501; AMP-binding; 3.
Pfam; PF00550; pp-binding; 3.
Pfam; PF00568; Condensation; 4.
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Qy 203	ETPESSDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLNDL-NASVFP 249	٥y	1193 SD
Db 173	ANGQGKPYSDYIKWLGKQDNE-EAESYWSERLAGFEQPSVLPGRLPVKKDEYVN	qu	1140 RE
Qy 250	)HLSDHLMVPNPTTAE-HRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFGA 304	δy	1253 NQ
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0y 305	VTEQSLPFDKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISSYD	Qy	1312 TD
Db 277		qa	1249 AD
Qy 350	DRLGHLAPFGLRDIRNTGDNGSAACDFOTVLLVTDGSHVNNGINGFLODIT	οy	1372 VIO
- Db 336	IQKRSALDGNLLNHLVAFENYPLDQELENGSMEDRLGFSIK	qa	1309 IV
Qy . 401	ESSHFMPCNNRALLLHCOMESSGALLVAXVDHNVIDSLOTTRIJOOFGHI	ΟŊ	1432 RV
		qa	1369 EL
Qy 451	IKCLOSPLDLSSWAEVNLM-TEYDRAEIESWNSOPLFVODTI-IHHEMI-KAVSHSPTK	Qy	1485 ME
	TRWMEAAVDQPAAFVREYGLVGDEBORGIVEVFNSTKAELPEGMAVHOVFEBOAKRTPAS	qa	1421 LSI
Qy 507	TAIOAWDGDWTYSELDNYSSRLAVHIKSLGLRAOOAIIPVYFFKSKWYTASMIAVIKSGN	QY	1545 TLI
		qa	1478 SA
Qy 567		Qy	1605 LR
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622	ASDDFSSLTKSODLAYVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALOFG	Qy	1665 VL
Db 595	AADNINLPSAPSDLAYIMYTSGSTGKPKGVMIEHKSILR-LVKNAGYVPYTEEDAMAOTG	do ,	1597 AV
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879	MAEHVTEAAVIIRKNKADENEICAYFAVSEIRRTIS	qq	1868 ERF
964	VLPRHSIPSFYICMLELPRTATGKIDRRELRIMGKDILDKOTOGA IVOOADAPIPVFA	Qy	1990 SSV
922		Dp	1926 SG
		QY	2050 DPS

-DTAAKLHSIWVQSLGIDPATVNVGAT--FFELGGNSITAIKM-VNMARSVGMDLKVSN 1076 YQHPTLAGISAVVK----GDPLSYTLIPKSTHEGPVEQSYSQGRLWFLDQLDVGSLWYL 1132 TESEKKLAEIWEGILG----VKAGVTDNFFMIGGHSLKAMMMTAKIQEHFHKEVPIKV 1021 :: ||: :: :: :: :: | :|| :: |
FERPTIQELALYLEENESKEEQFFEPIRQASYQQHYPVSPAQRRMYILNQLGQANTSYN 1081 PYAVRMRGPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCG 1192 DLDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDL 1252 DFERPAERSFAGERVMFGLDKQITAQIKSLMAETDTTMYMFLLAAFNVLLSKYASQDDI 1308 EFHLFQETDSLKGSVNFADELFKMETVENVRVFFEILRNGLQSSRTPVSILPLTDGIV 1544 TGRPKGVMIEHRVIIRTVTSGCIPNYPS--------ETRMAHMATIAFDGAS 1766 OMFPVLLGGGBEHIVQKETYTAPDBIAHYIKEHGITYIKLTPSLFHTIVNTASFAFDAN 1758 DFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDA 1371 IGTPIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFE 1431 VVSALQPGSRDLSSTPLAQLIFAVHSQK-----DLGRFKFQGLESVPVPSKAYTRFD 1484 LEKLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGW 1604 LIGHDTAPPDIEVTNVEFVRIRDALNDSNADG...FEVIEHDSTKPSATSLAYVLYTSG 1721 SIYSALLFGRTLVCV--DYMTTLDARA------LKDVFFREHVNAASHVTSSS 1812 OVPLRVPRRLSRTLMFFFLVVTDSTAPDALDAQGLYQGVQCYNGYGPTENGVMSTIYPI 1872 --STESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDK-ALDE 1929 REVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRD 1989 SVRDAAVVLQQNEDQAPEILGFVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIGEI 2049 RRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTI 1664 DPSTIGSDFKGWISMYDGSQIDFDEMHEWLGETTRTLHDNRSLGNVLEIGTGSGMILFNL 2109 ::: |||| :| |: :| | 3IQE-AVVLAVSEGGLQELCAYYTSDQD------

2110 DS: 1954 2170 IQ: 1954 2230 KM 1954 2290 LG	DSRLESYVGLEPSRSAAAFVNKATESIPSLAGKAKVQVGTATDIGQVDDLHPDLVVLNSV 2169  IQXFPSSSEYLAEIADTLIHLPNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQ 2229  ***CMAELEDMEEELLVEPAFFTSLKDRFPGLVPHVEILPKNMEAVNELSAXRYAAVVHVRGS 2289	RESULT 7 PPS2_BACE ID PPS2 AC P398
	195 222 195 228	ID
	222 195 228	
	195	1 6
	228	100
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	1953	800
1954	LGDELVLPVEKDDWIDFQANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAFERQVVASLN 2349	R CX
	:   1EK	RC
2350 SI	SNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSARQWSQNGALDAVFHHCCS 2409	RA RA
1957	1956	RA
2410 QC 1957 -	QGRTLVNFPTDHHLRGSDLLTNRPLQRLQNRRIAIEVRERLRSLLPSYMIPSNIVVLDKM 2469  : :     :  :   :	RL RN RN RP
0 0	SRRAKVVPKQQTAAPLPTFPISEVEVILCEEATEVFGMKVDITDHFF	RX RX RA
283		RA RA
2530 NJ 2002 Q	NLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIRQGLGLQQPVSDGQQQDR 2589    :  QSGGKAL	RA RA
2590 87	SAHWAPRTETEAILCDEFAKVLGFQ-VGITDNFFDLGGHSLMATKLAVRIGHRLDTTVSV 2648	RA RA RA RA
2649 KI	NLVQSKTNEIVGGREMAEYSPFQLLFTEDPEEFMASEIKPQLE 2	RA RA
2066 K	KALFEQPTVRQLAAYMEASAVSGGHQVLKPADK 2098	RA
2709 L( 2099 -	LQEIIQDIYPSTQMQKAFLEDHTTARPRFVPFYIDFPSTSEPDAAGLIKACE 2761                         1	RA RA
2762 - 2143 E	SLVNHLDIFRTVFAEASGELYQVVLSCLDLPIQVIET-EDNINTAINEFLDEFAKEP 2817                       : : :         :         LTPQLVNRHESLRTSFMEANGEPVQRIIEKAEVDLHVFEAKEDEADQKIKEFIRPFDLND 2202	RA RA RA
2818 V)	VRLGHPLIRFIIIK-OTKSMRVIMRISHALVDGLSLEHVVRKLHMLVNGRSLLPPHQ 2873      :::::::: ::  :  -  -	RA RA RA
874 F	SRYMOYTADGRESGHGFWRDVIONTPWTILSDDTV-VDGNDAT 291	RA RA
2259 D	DFAVWQNEAEQKERMKEHEAYWMSVLSGELPELDLPLDYARPPVQSFKGDTIRFRTGSET 2318	RT
2917 CI 2319 AI	CKALHLSKIVNIPSQVLRGSSNIITQATVFNAACALVLSRESDSKDVVFGRIVSGRGGLP 2976      :  :     :     :     :     start	28888
2977 VI 1 2368 V	EYQDIVGPCTNAVPVRAHI-ESSDYNQLLHDIQDQYLLSLPHETIGFSDLKRNCTDWPE 3035	
3036 A 2425 DI	AITNFSCCITYHNFEYHPESQFEQQRVEMGVLTKFVNIEMDEPLYDLAIAGEVEPDG 3092 ::	2888
3093 A	AGLKVTVIAKTQLFGRKRVEHLLEEVSKTFEGL 3125   ::	200

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groni A., Franchi E., Magistrelli C., Colombo E., Cosmina P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
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ture 390:249-256(1997).
- COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINES
- COFACTOR: LONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINES
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Steria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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2478 IGLQLEY - - ATDLFAKETAEKWSEYVLRLLKAV 2508
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Last annotation update)
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                                                                                                                                                                                                                 STANDARD;
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		900 ELVAXIVPEKGNSLPDLYQH 988 IDRRKLRIMGKDILDKOTQGAIVQQAPA :	FFELGGNSI   :     : FFQLGGQSL			1224 LGEDDHILTIVMHHIISDGWSIDVLRRD :  :                           : 1169 MGNNRGFLLLDMHHIIADGVSMSTLVQE	1284 QKDQFIEQEKQLNYWKKQLKDSSPA-  ::::::		1401 NIDHHDTFGTLINQVKATTTAAFENEDI 	1461 DLGRFKFQGLE-SVPVPSKAYTRFDMEF                 : :  :   1399 DF-RFEVPGLSISSVTPKHDISKFDLTL	1520 FEILRNGLQSSRTPVSILPLTDGIV   ::: : :   :  :  : :   1458 IELVKGVTADTEMRISNMOLLPAAERRL		1637 NLAYLPLDVRSPSARVQDILGGLSGPTI      :     :: ::   1574 GGAYLPIDPEYPKERISFMLND-SGAKL		1754 MAHMATIAPDGASYEIYSALLFGRTLVC :   :    :	1814 DVPLRVPRRLSRTLMFFFLVVTDSTAPD    1:	1856 NGYGPTENGVMSTIYPIDSTESFINGVP
QY Db	oy Oy	9	Qy	Qy	d d	oy da	Qy Dp	QY	Qý Dp	Qy Dp	oy .	Oy Dp	δγ Dp	Qy Dp	Qy Qp	Oy Dp	Οy
EMBL; 234 EMBL; 299 HSSP; P14 Subtilist	PR000873; AMP PR001242; Con PR003880; Ppa 01; AMP-bindi 50; pp-bindin 68; Condensat	PRINTS; PR001 PROSITE; PS00 PROSITE; PS00 PROSITE; PS50 Multifunction	Complete proteome.  DOMAIN 970 1037  DOMAIN 2007 2077  BINDING 2041 2041  SEQUENCE 2560 A8: 290	Query Match 11.0%; Pest Local Similarity 21.5%; Matches 671; Conservative 501	Qy 169 VWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPESSDATDTDSQSVSVVSMSCEDN 228	Qy 229 AVSATHFWQTHLNDL-NASVFPHLSDHLMVPNPTTTAEHRITFPLSQK 275 :  :  :  :  :   :   :   :     :       :	276 ALSNSAICRTALSILLSRYTHSDEALFGAV-TEOSLPFDKHYLADGTYQTVAPLR	330 VHCQSNLRASDVMDAISSYDDRLGHLAPFGLRDIRNTGDNGSAACDFQTVLLVTDGSHVN : : : : : : : : : : : : : : : : : : :	QY 390 NGINGFLQQITESSHFMPCNNRALLLHCQMESSGALLVAYYDHNVI- 435	436	479 SWNSQPLEVQDTLIHHEMLKAVSHSPTKTALQAWDGDWTYSELDNVSSRLAVHIKSLGLR :   : :   : :     : : :     : : :	AQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVALTSKLH	Qy 599 RETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQDLAYVIFTSGS 644	Qy 645 TGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGCCVCI 704	QY 705 PSDDDRMNSIPSFINRYNVNWMMATPSYMGTFSPEDVPGLATLVLVGEQMSS 756   1	Oy 757 -SVNAIWAPKLQLLNGYQGSESSICFASNMSTEPNNMGRAVGAHSWVIDPNDI 809 1	

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g G	845	ALTO THE TOTAL TO THE TRANSPORTED THE TOTAL TO THE TRANSPORTED	89
٥y	928	TKAI	987
qq	900	ELVAYIVPEKGNSLPDLYQHLAGTLPSYMIPASIINISQMPLTSSGK	946
οy	988	VFADT	1047
qq	947	RFALPEPENNTSVTYMAPRTL	992
δy	1048	FFELGONSITALKMVN-MARSVGMDLKVSNIYOHPTLAGISAVVKGDPLSYTLIPKS	110
qq	993	FFQLGGGSLKAAALVSRIHKKLNVELPLSEVFSYPTVESMAVKLMSLKEHAFTQIEPA	105
٥y	1104	THEGPVEOSYSQGRLWFLDQLDVGSLWYLIPYAVRMGPVNVDALRRALAALEQRHETLR	116
qq	1051	DORDVYPLSFSOKRLYALHQLADDSTGYNMPAVLELRGNLNRQRLRSVLTELVNRHEALR	111
λο i	16	TTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLSSEAGMRATLLR	122
QQ	1111	TVFVLDRDEPVQIIYPEMAFDLKELEMESEQMLESAIETFIKPFYLSSGPLFRACVIT	116
Qy Db	1224	LGEDDHILTIVMHHIISDGWSIDVLRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKW :  :             :	1283 1219
0y	1284	QKDQFIEQEKQLNYWKKQLKDSSPA-KIPTDFARPALLSGDAGCVHVTIDGELYQSLR	1340
qq	1220		1279
δy	1341	AFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNFPELEDIIGCFVNTQCMRI	1400
qa	1280	RLMAETGTTLYMILLAVYSILLSKLSGQEDIVVGSPAAGRPHADLERVIGMFVNTLAMRS	1339
Qy	1401	NIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGSRDLSSTPLAQLIFAVHSQK	1460
qa	1340	KPEGHKTFSSYLHDIRHLALTAYEHQDYPFEELADKLDT-NREVNRNPLFDAMLVLQSSE	1398
Qy	1461	DLGRFKEGGLE-SVPVPSKAYTRFDMEFHLFQETDSLKGSVNFADELFKMETVENVRVF	1519
Db	1399	DF-RFEVPGLSISSVTPKHDISKFDLTLHAEEHLSGIRCRFEYSTALFEEETITQWASYF	1457
Qy	1520	FEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHVDYPRESSLADVFQTQVSAY	1576
qa	1458	NWO	1513
Qy	1577	PDSLAVVDSSCRLTYTELDRQSDILAGWLRRSMPAETLVAVFAPRSCETIVAFFGVLKA	1636
qa	1514	PEHIAVVCGHSQLTYRDLNERAERAAAMLIKQGVRTGDIVGLMLDRSPDMIIGVLSILKA	1573
Qy	1637	NLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNAD	1696
qa	1574	GGAYLPIDPEYPKERISFMLND-SGAKLLLTERGLNKPADYTGHILYIDECENNSIPA	1630
Qγ	1697	GFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETR	1753
Db	1631	DVNIEEIVTDQPAYVIYTSGTTGQPKGVIVEHRNVISLLKHQNLPFEFNHEDVWT	1685
QY	1754	MAHMATIAFDGASYEIYSALLEGRTIVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQ	18
qa	1686	LFHSYCFDFSVWEMFGALLNGSTLVVVSKETARDPQAFRLLLKKERVTVLNQTPTA	1741
Qy	1814	RLSRTL	1855
qa	1742	FYGLMLEDQNHTDHLNIRYVIFGGEALQPGLLQSWNEKYPHTDLI	1786
Oy	1856	NGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTG	1915

			2298 DNDAASNTFKDTEVIDFELSRHHTELLLTAAHKAYSTEMNDILLTALGLALQK 2350 2957 ESDSKDVVFGRIVSGRQGLPVEYQDIVGPCTNAVPVRAHIESSDYNQLLHD 3007 301 IN THE STANDARD SHERNER STANDARD SHERE ERLGHLIKQ 2410 3008 IQDQVLLSLPHETIGFSDLKRNCTDWPEAITNFSCCITYHNPEYHPESQ-FEQQ 3060 301 IQDQVLLSLPHETIGFSDLKRNCTDWPEAITNFSCCITYHNPEYHPESQ-FEQQ 3060 301 IN TKDM-LHRIPHKGAGYGVLKYISKRMGSQKNSPEISFNYLGQFDQDIQSNAFEVS 2464 3051 RVEMGVLTKFVNIEMDEPLYALBAGGVEPDGAGLKVTVIAKTQLFGRKRVEHLLEEVSK 3120 3051 RVEMGVLTKFVNIEMDEPLYALBISGAVSSGCLNMHIIYNRFQFEEKTIQTFSRHFKQ 2518 3121 TFEGL 3125 2519 TLENI 2523
Qy Db	2153 IGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVRSQATNEHFLAA 2212	SUL SB_	T 8 BACBR GRSB_BACBR STANDARD; PRT; 4451 AA.
Qy Db	2213 RAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAV 2272 1941 1940	AC P14 DT 01- DT 01- DT 16-	P14688; 01-APR-1990 (Rel. 14, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Gramicidin S evetherase II [Includes APP-dependent proline adenylase
Oy Dp	2273 NELSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLKSSDAAIMAVSK 2332 		ne activase); ATP-dependent valine adenylase (Vase); ATP-dependent ornithine adenylase (OrnA) (P-dependent leucine adenylase (LeuA) (Leucine a
Qy Dp	2333 IPFEITAFERQVVASLNSNIDEWOLSTIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSAR 2392 		GRSB OR GRS2. Bacillus brevis. Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus. NCBL_TaxID=1393;
Oy Dp	2393 OWSONGALDAVFHHCCSOGRTLVNFPTDHHLRGSDLLTNRPLORLONRRIAIEVRERLRS 2452 ::    :: 1955DIRTYLKN 1962	RN [1] RP SEQ RC STR RX MED	(1) SERDINER FROM N.A STRAINE-ATCC 9999; MEDLINE-9219998; Pubmed-1560782;
Oy Dp	2453 LLPSYMIPSNIVVLDKMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCE 2512       :  : : ::    :        :        :     1963 ALPDFMLPARMIQIDSIPVTVNGKLDQKALPEPEKQA		Turgay K., Krause M., Marahiel M.A.; Four homologous domains in the primary structure of GrsB are related to domains in a superfamily of adenylate-forming enzymes."; Mol. Microbiol. 6:529-546(1992).
Qy Dp	2513 EATEVFGMKVDITDHFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIR 2572 2000		2  SEQUENCE OF 1-948 FROM N.A. STATAIN-NAGANO; MEDLINE-92041751; Pubmed=1939016;
O,	QGLGLQQPVSDGQGQDRSAHMAPRTETEAILCDEFAKVLGF-QVGTTDNFFDLGGHSLMA :		Hori K., Yamamoto Y., Tokita K., Saito F., Kurotsu T., Kanda M., Kanura K., Furuyama J., Saito Y.; "The nucleotide sequence for a proline-activating domain of gramicidin S synthetase 2 gene from Bacillus brevis.";
O O O	2632 TKLAVRIGHR-LDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAEYSPFQLL 2690 :		
Qy Db	2691 FTEDPEEFMASEIKPQLELQEIIQDIYPSTQMQKAFLFDHTTARPRPFVPFYIDFPSTSE 2750	RX MED RA Kra RT "Gr	000087 nmar J lin S grsB
Qy Dp	2751 PDAAGLIKACESLVNHLDIFRTVFAEASGELYQVVLSCLDLPIQVIETEDNINT 2804		to fatty acid thioesterases.";  Bacteriol. 171:5422-5429(1989).  [4]  SEQUENCE OF 1-15, AND CHARACTERIZATION.
o, do	2805 ATNEFLDEFAKEPVRL-GHPLIRFTIIKQTKSMRVIMRISHALYDGLSLEHVVRKLH 2860 	RC STR RX MED RA KUI	STRAIN=Wagano; MEDLINE-92011463; PubMed-1917901; Kurotsu T., Hori K., Kanda M., Saito Y.; "Characterization and location of the L-proline activating fragment
Qy Db	2861 MLYNGRSLLPPHQFSRYMQYTADGRESGHGFWRDVIONTPWTILSD 2906		from the multifunctional gramicidin S synthetase 2."; J. Biochem. 109:763-769(1991)!- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME, ABLE TO ACTIVATE AND POLYMERIZE THE AMINO ACIDS PRO, VAL, ORN AND LEU.
ολ	2907 DTVVDGNDATCKALHLSKIVNIPSQVLRGSSNIITQATVFNAACALVLSR 2956	<del></del>	ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS COFACTOR: CONTAINS 4 COVALENTLY BOUND PHOSPHOPANTETHEINES PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF THE CYCLIC REPTIDE

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.008 AIVQQAPAPIPVFADTAAKLHSIWVQSLGIDPATVNVGATFFELGGNSITAIKMVN-MAR 1066
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                          KKC--QLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPESSDATDTDSQSVSVV
                                                                                                                                                                434 VIDSLQTTRLLQQFGHLIK---CL-QSPLDLSSMAEVNLMTEYDRAE-IESWNSQPLEVQ
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                                                                                                                                                                                                                                                                            245 RIANQSQVTLNIVFQTIWGIVLQKYNSTNHVVYGSVV-SGRPSEISGIEKMVGLFINTLP
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                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
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ANTIBIOTIC GRAMICIDIN S (D-PHE-PRO-VAL-ORN-LEU)2.
SUBUNIT: LARGE MULTIENZYME COMPLEX OF GRSA AND GRSB.
DOMAIN: CONSISTS OF FOUR MODULES, AND HARBORS A PUTATIVE
THIOGESTERASE DOMAIN AT ITS C-FERMINAL END. EACH MODULE.
INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE
ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITIATION
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DOMAIN 2 (VALINE-ACTIVATING)
DOMAIN 3 (ORNITHINE-ACTIVATING)
DOMAIN 4 (LEUCINE-ACTIVATING)
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PROSITE; PS00012; PHOSPHOPANTETHEINE; 4.
PROSITE; PS00455; AMP BINDING; 4.
PROSITE; PS50075; ACP_DOMAIN; 4.
Ligase; Antibiotic blosynthesis; Multifunctional enzyme; Repeat; Phosphopantetheine; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVRLHL -> QLPLTP (IN REF. 2 MW; E0029C9B51F5A4B7 CRC64;
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ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 4.
PHOSPHOPANTETHEINE (BY
PHOSPHOPANTETHEINE (BY
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                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 4 ACYL CARRIER DOMAINS
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K -> R (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condonsath:
InterPro; IPR003809; Ppantne_attach.
InterPro; IPR003199; Ser_estrs_site.
InterPro; IPR001031; Thioesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00668; Condensation; 4. PF00975; Thioesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00501; AMP-binding; 4. Pfam; PF00550; pp-binding; 4.
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EMBL; X09703; AAA58719.1; -.
EMBL; X15577; CAA33604.1; -.
EMBL; DO0938; BAA00778.1; -.
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HSSP; P14687; 1AMU.
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	: :: :       :	SDGWSIDVLRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFTEQEKQ        :: :: :	LNYWKKQLKDSSPAKIPTDFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFV	VLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDIIGCFVNTQCMRINIDHHDFFGTLI :	NQVKATTTAAFENEDIPFERVVSALQPG-SRDLSSTPLAQLIFAVHSQKDLGRFKFQGLE	SVP-VPSKAYTREDMEFHLEQETDSLKGSVNFADELFKMETVENVVRVFFEILRNGLQSS	RTPVSILPLTDGIVTLEKLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSC		PSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHD  :	STKPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETRMAHMATIAFDG	COASDLATIMYISSSIGATAGGONG HARNYIAKLYKNYNYVQVREDDKIIQTGAIGEDA ASYBIYSALLFGRILVCUDYMTILDARALKDVFFREHVNAASHVTSSSODVPLRVPRILS :::!!	RTLMFFFLVVTDSTAPDAL-DAQGLYQGVQCYNGYGPTENGVNSTIXPIDSTES	FINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDK-ALDENREVHIT :::   -  -  -  -  -  -  -  -  -  -  -  -	VNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESABIEAALLRDSSVRDAA  -	VVLQQNEDQAPEILGEVVABHD		ROALPERFOGEFG TATEST VAPSSSD LEMKLAELWHNVLGVNKIGVLDNFFELGGGBSLKAMIM	IGSDERGWISMYDGSQIDFDE:GETTRILHD	ALTEROGRATION FOR METABORDI LORGE ELGANS LONG HEALDEN SEE VORVHU  NRSLGNVLEIGTGSGMILENLDSR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: ACTIVATES TWO AMINO ACIDS AND INCORPORATE A D-ORNITHINE FROM ITS SECOND ACTIVE SITE INVO BACITAGALIN.
- FROM ITS CATALYTIC ACTIVITY: L-ORNITHINE = D-ORNITHINE.
- - - COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marahiel M.A.;
Bacillus licheniformis ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Konz D., Klens A., Schoergendorfer K., Marahiel M.A.;
"The bacitracin biosynthesis operon of Bacillus licheniformis ATC
10716: molecular characterization of three multi-modular peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3071 VNI--EMDEPLYDLAIAGEV--EPDGAGLKVTVIAKTQLFGRKRVEHLLE 3116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDLVSKLEHAKFDLSLVAVVFEEEIAFGLQYC----TKLYKEKTVEQLAQ 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Jul. 1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bacitracin synthetase 2 (BA2) [Includes: AFP-dependent lysine adenylase (Lysh activase); AFP-dependent D-ornithine adenylase (D-OrnA) (D-ornithine activase); Ornithine racemase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis.
Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECTION STATES SECTION IN STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE 
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STRAIN-ATCC 10716;
MEDLINE-98089193; Pubmed-9427658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  HETIGESDL ---
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Chem. Biol.
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SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                          EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---DIDISRFALAWKEIVNQTPALRAFTSDSGKTSQVILKDSFVFSWMCWSSSSSPDE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------EFRLEYS---ELGDQSIQEKI-SRFIKPFELEK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WQRDIEQQSRLKKQEAYWLNTFRGDI-PVLNMPLDFPRPKIRSFQGNRTVVELDQDTTKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKTIAAKNGVTMYMLLLAGYTILLSKYTGQEDIIVGS-----PIAGRPHADLNGTIGMF 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCQMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMA--EVNLMTEYD 473
                                                                                                                                                                                                          ween the Swiss Institute of Bioinformatics and the EMBL outstati
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R HSSP, P14687; 1AMU.

R HSSP, P14687; 1AMU.

R InterPro; 1PR001243; AMP-bind.

InterPro; 1PR001242; Condensatn.

InterPro; 1PR0013880; Ppantne_attach.

R InterPro; 1PR0013880; Poantne_attach.

R Ffam; PF00550; Pp-binding; 2.

R Ffam; PF00550; Pp-binding; 2.

R PF1 PF00550; Pp-binding; 3.

R PF005TE; PS001012; PHOSPHOPANTETHEINE; 1.

R PROSTIE; PS00455; AMP_BINING; 2.

R Milese; Incomerses, Antibioctic biosynthesis; Phosphopantetheine; Milest Processes.
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ACYL CARRIER (ACP) 2.

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

W; FP654FAC5B8BBA6F CRC64;
SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN 1 (LYSINE-ACTIVATING), DOMAIN 2 (D-ORNITHINE-ACTIVATING)
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; Mismatches 1051;
                                                                                 SIMILARITY: CONTAINS 2 ACYL CARRIER DOMAINS.
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474 RAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTALQAWDGDWT 517   1   1   1   1   1   1   1   1   1	Qy	1510 ETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHVDYPRESSLA 1566
YSELDNVSSRLAVHIKSLGLRAQOAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPP	γος dα	1567 DVFOTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAVFAPRSCET 1626 1: :     :
ARTAQVVTQTRATVALTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLFKSQDLAY   : : :   : : :   : : :       : : :	O <sub>Y</sub>	1627 IVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRI 1686 : :
VIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTLI   :    :    :    VIYTSGSSGRPKGVMTTHRNVVHXVDAFTKRIPLSEHDTVLQVVSFSFDAFSBEVYPILA	Oy Dp	1687 RDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTS 1742 :::  ::  :
	Qy	1743 GCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARAL 1793 :
VLVGEQMSSSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRAVGAHSW	Qy	1794 KDVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDAQGLY- 1849  : : :    :    :   1775 YDMINKYGIHMLESTPSLIIPLMKYIDHHKLDFSSMKLLIMGSDTCTIKDYKMLVE 1830
/02 VLAFELVENTINGADVINSIGPTEATVCATITQLSSALKRATSIFICKFLSNYK- 835  803 VIDPNDINKLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKL 862  803 VVIANOVGEDODOVAVGETITGGGGARDYINDENTINGARANINGARA	Qy	1850GGVQCYNGXGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVDPEQQLVG 1904   ::
YRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIVVEATKRSQ	Qy	1905 IGVMGELVVTGDGLARGYSDK-ALDENRFVHITVNDQTVKAYRTGDRVRYRIGDGLIE 1961 
886 TRIGDLAKMESDGNIBELGKIDSQVRIKGYRIELEELEHRELMNDNINEALVVAREDQ 943 923 SANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICMLELPR 982	δο.	1962 FFGRMDTQFKIRGNRIESABIEAALLRDSSVRDAAVVLQQNEDQAPBILGFVVADHDHSB 2021 
TATGKIDRRKLRIMGKDILDKOTOGAIVQQAPAPIPVFADTAAKIHSIWVQSLGIDPA-T	Q <sub>Y</sub>	2022 NDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGE 2081 :
1042 VNVGATFFELGGNSITAIKMVNMARS-VGMDLKVSNIYQHPTLAGISAVVKGD 1093	QY	2082 TTRTLHDNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEPSRSAAAFVNKATESIPSLAG 2141
IGINDHFFDIGGHSLKAFSMAAKIQSALKVEVTLKEIFNHSTIODLAAYIAQKQKQVQSD	7 V	KAKVQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVR
1094 PLSYTLIRKSTHEGFVEQRYSGGRUWFLDOLDVGSLWYLIPYAVRNGGPVNVDALRRALA 1153 1098IOKABKKEYYPLSSAQKRIZILAOJEBGGTAYNWPRAMKIKGELOTDKARRRR 1151	qa	1993 1992
ALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLSS	Qy Dp	2202 SQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRFPGLVEH 2261 1993
1152 TLIKRHESSRTSFVTINGEPVQNINEEVTFEMKYRELDNCSLRERMNQ-FIRPFELEK 1208 1214 EAGWRATLLRLGEDDHILTIVWHHIISDGWSIDVLRRDLNQLYSAALKDSKDPLSALTPL 1273	Qy	VEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLK
1209 APLLRAELVRVNAAEHILLLDMHHIISDGVSIGILMKEWAALVEEKELAPL 1259	q m	1993
1274 PIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSPA-KIPTDFARPALLSGDAGCVHVT 1330       :::  :  : :     ::            ::     1260 KIQYKDYSEWQRDPWQKDRLKKQEESWLSVFONDIPVLNMPTDFPRPOMOSYEGDRIAFA 1319	දි <u>අ</u>	
IDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDIIG 1	QY	2382 AGFRVEVSSARQWSQNGALDAVFHHCCSQGRTLVNFPTDHHLRGSDLITNRPLQRLQNRR 2441 2005
1391 CEVUTQCMRINIDHHDTEGTLINQVKATTTAAFENEDIFFERVVSALQPGSRDLSSTPLA 1450	QY	2442 IAIEVRERLRSLLPSYMIPSNIVVLDKMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTF 2501  :
MFVGTLAMRNHPKGGRTFIEYLQDVKENTFNAYENQDYPFDELVDKLDL-ERDISRNALF	QY	PISEVEVILCEBATEVEGMKVDITDHFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDH
1431 QLLFAVHSQKDLGKFRFQGLESVPVPSK-AYTRFDMEFHLFQETDSEKGSNRFADELEKM 1509 	qa	2046EPAGDVIA
	o <sub>y</sub>	2562 PVFADLASVIRQGLGLQQPVSDGQGQDRSAHMAPRTETEAILCDEFAKVLG-FQVGITDN 2620

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803
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                                                                            -VPLTPVQRSF-----YRENGFAE
                                                                                             FYIDFPSTSEPDAAGLIKACESLVNHLDIFRTVFAEASGELYQ----VVLSCLDLPIQVI
                                                                                                                               ETEDNINTATNEFLDEFAKEPVRLGHPLIRFTIIKQTKSMRVIMRISHALYDGLSLEHVV
                                                                                                                                                                  RKLHMLY----NGRSLLPPHQFSRYMQYTADGRESGHG------FWRDVIQNTPMTIL
                                                                                                                                                                                  EDFEAAYGQALQGKPIELGYKTDSYKTFSEKLAEYANSKKLLKEQEYWREISKGKMAFLP
                                                                                                                                                                                                                                      2964 VFGRIVSGRQGLPVEYQDI ---- VGPCTNAVPVRAHIESSDYNQLLHDIQDQYLLSLPH
                         FFDLGGHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGRE
                                                                                                                                                 KTEKNLEKTVYQIATNIQKDISISEGKMIKLCVFKTTEGDHLLIAIHHLLVDGVSWRILF
                                                                                                                                                                                                    SDDTVVDGNDATCKALHLSKIVNIPSQVLRGSSNII-TQATVFNAACALVLSRESDSKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ARCC 90305 / SB111;
MEDLINE-93100328, PubMed-128148;
Scott-Craig J.S., Panaccione D.G., Pocard J.-A., Walton J.D.;
"The cyclic peptide synthetase catalyzing HC-toxin production in if illamentows fungus Cochliobolus carbonum is encoded by a 15.7-kilobase open reading frame.";
J. Biol. Chem. 267:26044-26049(1992).
                                                                                                                                                                                                                                                                                                                                                                                                           Dothideomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from L-Ala by TOXG. COFACTOR: CONTAINS 4 COVALENTLY BOUND PHOSPHOPANTETHEINES.
                                                                                                                                                                                                                                                                                                                                                                                                 Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fundi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5017;
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                                                                                                                                                                                                                                                                                                                                      5217 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 90305 / SB111;
MEDLINE=20138231; PubMed=10671527;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by. non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                 SIMILARITY: CONTAINS 4 ACYL CARRIER DOMAINS. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF HC-TOXIN.
SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
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PHOSPHOPANTETHEINE (BY SIMILARITY).
W; 0331D9C5400163A5 CRC64;
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InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR001380; Ppantne_attach.
Ffam; PF00501; AMP-binding; 4.
Pfam; PF00668; Condensation; 5.
PRINTS; PR00154; AMPBINDING.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 4.
PROSITE; PS00075; ACP_DOMAIN; 3.
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  ---MHVLNI 3461
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                                                        2471 LNANGKVDRKELSRRAKVVPKQQTAAPLP-TFPISEVEVILCEEATEVFGMKVDITDHFF
                                                                                               2530 NLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIRQGLG-*-LQQPVSDGQG
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MEDLINE=93360813; PubMed=8355609;
Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
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Zuber P., Yamane K.;
  -VSLMRSWDS--
                                                                   01-AUG-1992 (Rel. 23, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Surfactin synthetase subunit 1.
SRFAA OR SRFAI OR SRFA.
Bacillus subtilis.
Bacillus subtilis.
Bacteria: Firmicutes; Bacillales; Bacillus.
NCBI_TaxID=1423;
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  -Ardi---
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                                       3462 ANTSENLOT
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Venema G., van Sinderen D.;
"Sequence and analysis of the genetic locus responsible for surfactin
synthesis in Bacillus subtilis.";
Mol. Microbiol. 8:821-831(1993).
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                                                                                                                                                                                                                                            Yamane K., Kumano M., Kurita K.; Time 25 degrees 756 degrees region of the Bacillus subtilis chromosome: determination of the sequence of a 146 kb segment and identification of 113 genes."; Microbiology 142:3047-3056(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "srfA is an operon required for surfactin production, competenc development, and efficient sporulation in Bacillus subtilis."; J. Bacteriol. 173:1770-1778(1991).
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Nakano M.M., Magnuson R., Myers A.M., Curry J., Grossman A.D.,
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PROSITE; PSO0012; PHOSPHOPANTETHEINE;
PROSITE; PSO0455; AMP_BINDING; 3.
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InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR003880; Ppantne_attach.
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Pfam; PF00550; pp-binding; 3.
Pfam; PF00668; Condensation; 4.
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235 FWQTHLNDLNASVFPHL-SDHLMVPNPTTTAEHRITFPLSQKALSNSAICRT 285	389 NNGINGFLQOITESSHFMPCNNRALLLHCQMESSGALLVAYYDHNVIDSLQTTRLLQOFG	942 AIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPARTAQVYTQTRATVALT-SKLHR-599 11   1   1   1   1   1   1   1   1   1	767QLLINGYQQSESSSICF-ASNMSTEPNNMGRAVGAHS-WVIDPNDIN  1	991 RRLRIMGKDILDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLGIDPATVNVGATFFE 1050
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AYDHFEDIGGHSLAGMKMLALVHQEL 2059 GGREMAEYSPFQLLFTEDPEEFMASE 2702 LSLEHVVRKLHMLYNGRSLLPPH-QF 2874 SQFEQQRVEMGVLTKFVNIEMDEPLY 3080 TARPRPFVPFYIDFPSTSEPDAAGLI 2757 PIQVIETEDNINTATNEFLDEFAKEP 2817 FLSKISGQDDIIVGSPVAGRS--QAD 2367 ODQYLLSLPHETIGFSDLKRNCTDWP 3034 LPTFPISEVEVILCEEATEVFGMKVD 2523 ASAEKG-----TAAS 2091 --F 2465 -----HLLEEVS 3119 ||: |: KQYWMELLDAVT 2509 --FERKTAK----ae; Bacillus. е

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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Brusslar L., Brains A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Dorizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Febret C., Ferraria E., Foulger D.,

RA Guiseppi G., Guy B.J., Hage K., Haiech J., Harwood C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Guiseppi G., Guy B.J., Maga K., Haiech J., Lazarevic V.,

RA Kuria K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kuria K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

Sakfuchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Takeuchi M., Tamakoshi A., Taragai T., Tarahashi H., Taramakoshi A., Taramaru K.,

RA Takeuchi M., Tamamoshi A., Taramat T.,

RA Takeuchi M., Tamamoshi A., Taramat T.,

RA Takeuchi M., Tamamoshi A., Taramat T.,

RA Winters P., Wahdat A., Yamamoto H., Vanier F., Vassarotti A.,

RA Winters P., Wahdat R., Sandeler E., Wedler H., Waitzenegger T.,

RA The Complete genome sequence of the Gram-positive bacterium Bacillus

R. The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                A putative new peptide synthase operon in Bacillus subtilis: partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
-!- COFACTOR: CONTAINS 1 COVALENTLY BOUND PHOSPHOPANTETHEINE
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PROSITE; PS50075; ACP_DOMAIN; 2.
Multifunctional enzyme; Ligase; Repeat; Phosphopantetheine;
Complete proteome.
                                                                   Pognoni A., Franchi E., Magistrelli C., Colombo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 2 ACYL CARRIER DOMAINS.
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InterPro; IPR003880; Ppantne_attach.
Pfam; PF00501; AMP-binding; 2.
Pfam; PF00550; pp-binding; 2.
Pfam; PF00668; Condensation; 3.
                                                                                                                                                                                                                                                    MEDLINE=98044033; PubMed=9384377;
                                             MEDLINE-95227362; PubMed-7711903
                                                                                                                                                           Microbiology 141:645-648(1995)
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InterPro; IPR000873; AMP-bind.
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PROSITE; PS00012; PHOSPHOPAN
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                                                                                                                 Gaps
                                                                                                              436;
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                                                                            9.9%; Score 1604; DB 1; Length 25
Local Similarity 24.9%; Pred. No. 1.7e-84; †
ies 611; Conservative 437; Mismatches 970; Indels
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Thu Jun

	Qy	1054 NSITAIKMVN-MARSVGMDLKVSNIYQHPTLAGISAVVK-GDPLSYTLIPKSTHEGPVEQ 1111	ī	
	qq	995 HSLKATALVSRIAKEFDVQVPLKDVFAHPTVEGLATVIREGTDSPYEAIKPAEKQETYPV 1054	qq	1995 PAPNNVLSRP
	QY	1112 SYSQGRLWFLDQLDVGSLWYLIPYAVRMRGPVNVDALRRALAALEQRHETLRTTFE-DQD 1170	δλ	2110 DSRLESYVGLE :     :
	Db	:     :       :       :	qa	2049 AARLAAEGWSN
•	۸O		ΟŊ	2159 LHPDLVVLNSV
-	연		qa	2109 FHYHYNQS
,	^0	.5 AGWRATLLRIGEDDHILTIVMHHIISDGWSIDVIRRDINOLYSAALKDSKDPLSALTELP	δλ	2206 NEHFL
	r qa		qq	2166 KDHELFGLYIS
J	۸ŏ	I LOYSDFAKWOKDOFIEOEKOLNYWKKOLKDSSPA-KIPTDFABPALLSGDAGCYH	Qy	2255 FPGLVEHVEII
-	<sub>.</sub> අ		Dp	2224 LLIALHHLVII
_	Oy .	1329 VTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDI 1388	QY	2314
_	qq	:   :    :    :    :        :	ΩP	2278 AESKQLLSEKI
	^O	9 IGGEVNTOCMRINIDHHDTEGTLINOVKATTTAAFENEDIPFERVVSALOPGSRDLSSTP	δy	2344V
_	- AG		QQ	2338 AYGTDANELLI
	Qy	1449 LAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTRFDMEFHLFQETDSLKGSVNF 1502	RESULT 1	r 13
ī	Db	: :  : : : : :   :   :   :   :   :   :	ACVS_C ID A	CEPAC ACVS_CEPAC STANI
_	Qy	1503 ADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHVDY 1559	AC DT	(Rel.
-	qo	:  :    :    :		01-MAY-1992 (Rel. 22 16-OCT-2001 (Rel. 40
	۸C	0 - PRESSLADVFOTOVSAYPDSLAVVDSSCRLTYTELDROSDIJAGMI.BBRSMPARTI.VAV	•	ha-ami
-	; q	4 AOKDIPFHRIFEAKAEENPEHTAVIDNETETSYRI, NERANRIARTIONRKOPKT-VAV		AB.
	, <u>}</u>	Q PADRSCRIVARECTIVITATION AND AND AND AND AND AND AND AND AND AN	388	Eukaryota; Fungi; As
	ැ දි	1		nypocreates; hypocre NCBI_TaxID=5044; [1]
_	ΛĊ	4 PDIEVINVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAVVLYTGGSTGRPKGVMIEH		SEQUENCE FROM N.A. MEDLINE=91177827: P.
_	· 42	2 PESERKHIT-FI,DAGGERESKICNIMI SDADEBOVITTWCGTTTGADGADGADGADGADGADGADGADGADGADGADGADGADG	-	N
		AUNICHT TEDENCOTE EEGING NEUNENTEER VIIITIOGIIGGENGIIG II II II I I I I I I I I I I I I I		characterization of encoding alpha-amino
۱ م	λ i	KVIIKIVISGCIPNYPSETRMAHMATIAFDGASYEIXSALLFGRTL	RT	
	qq	.QNFTHAALAWRQIYELDRKPVRLLQIASFSFDVFSGDLARTLTNGGTL		n .
`	ΣŽ	1780 VCVDYMTTLDARALKDVEFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFLVVTD 1836		[2] DAPHTAI SECHENCE EDG
-	QQ	1712 IVCPDETRLEPABIYKIIKSQRITVMESTPALIIPVMEYVYRNQFKLPDLDILILG 1767		STRAIN=ATCC 11550;
	2y	1837 STAPDALDAOGLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGR 1886	RA	MEDLINE=91168300; PU Hoskins J.A., O'Call
	qo	1768 SDMVKAQDFKTLTDRFGQSMRIINSYGVTEATIDSSFYETSMGGECTGDNVPIGS 1822		Chen V.J., Skatrud F "Gene disruption of
_	QY	VVTGDG		Cephalosporium acrem Curr. Genet. 18:523-
	q	1823 PLPNVHMYVLSQTDQIQPIGVAGELCIGGAGVAKGYHHKPDLTQMKFTENPFVS 1876	' 88	ACV ARE ACTIVATE
-	ογ	TOFKIRGNRIESAEIEAALLRDSSV	88	ജെ
I	qq	1877 GERLYRTGDRACW-LPNGTIRLGRMDYQVKINGYRIETEEIESVLLQTGLVREAAVAVQ 1935		- COFACTOR: CONTY (POTENTIAL).
	2y	2001 ONEDQAPEILGFVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTI 2054		- PATHWAY: FIR CEPHALOSPORI
	QD	1936 HDKNGQAGLAAYIVPS-DVNTNALRAALTKELPAYMIPAYLIPLVNMPLTLNGKLDRNAL 1994		SIMILARITY: FAMILY.
J	٥y	2055 GSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLHDNRSLGNVLEIGTGSGMILFNL 2109	D RO	-!- SIMILARITY: CONT PIR; A38531; YGCEVC.

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LEPSRSAAAF--VNKATESIPSLA-----GKAKVQVGTATDIGQVDD 2158
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                                                                                          SVIQYFPSSEYLAEIADTLI----- HLPNVQRIFFGDVRSQAT----- 2205
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                                                                                                                                                                                                                                         -----AARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDR 2254
                                                                                                                                                                                                                                                                                                                                                                                                                   -------KSLGDLLK-SSDAAIMAVSKIPFEITAFERQ- 2343
                                                                                                                                                                                                                                                                LIPKNMEAVNELSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQ-
                                                                                                                                                                                                                                                                                                                                                      (TYWQTILDAHTAFLPKDIENVPDKLQMNSDAAAFVLSGDWTEKLLFETQO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laghan N., Queener S.W., Cantwell C.A., Wood J.S.,
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OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE
IED AS AMINOACYL-ADENYLATES WITH-PEPTIDE BONDS
THE PARTICLPATION OF AMINO ACID THIOLESTER
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Ascomycota; Pezizomycotina; Sordariomycetes;
reaceae; mitosporic Hypocreaceae; Acremonium.
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(), Last annotation update)
noadipyl)-L-cysteinyl-D-valine synthetase
synthetase) (&CVS).
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f the pcbAB gene encoding ACV synthetase
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22; Last sequent 40, Last anno
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LSQAAIQPNKLVGLIMDKSEHMITSILAVWKTGGAYVPIDPRYPDQRIQYILEDTAALAV 1463
                                                                                                                                                                                                                                --AVVKGD-PLSYTLIPKSTHEGPVEQSYSOGRLWFLDQL----DVGSLWYLIPYAVRM 1139
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                                                                                                                                                                                                                                                                                                                    FDKIRETFPGLIINGYGPTEVSITTHKRPYPFPERRTDKSIGCQLDNSTSYVL--NDDMK 1694
                                                                                                                                                                                                          SDDDR--MNSIPSFINRYNVNWMMATPSYMGTFSPEDV-PGLATLVLVGEQMSSSVNAIW 762
                                                                            IMIEHR-----AFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCVCIP
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               (CYSTEINE-ACTIVATING).
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DOMAIN 3 (VALINE-ACTIVA
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                                                                                                                             TSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETRMAH -- -- MATIAFDGASYEIYSALL
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STRAIN=VAR LC 411;
MEDLINE=92065808; PubMed=1956290;
Coque J.J.R., Martin J.F., Calzada J.G., Liras P.;
The cephamycin blosynthetic genes pcbAB, encoding a large multidomain peptide synthetase, and pcbC of Nocardia lactamdurans arclustered together in an organization different from the same genes
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Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
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16-OCT-2001 (Rel. 40, Last annotation update)
Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine
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 There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 AWKEIVNOTPALR-AFAFTSDSGKTSQVILKDSFVFSWMCWSSSSSPDEVVRDEAAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWQAARQTYPALKLRFDWAEE---PVQIVDNDDKPFDWRFVDLSATADDAEQEARVRELO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ASGPRCNRFVLL---EDMQTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAICRTALSILLSRYTHS - - - - DEALFGA - VTEQSLPFDKHYLADGTYQTVAPLRVHCQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1128 QVTLHSVLQFVWHKVLHAIGGGNTTVVGTIVSGRNLPVDGIENSAGLFINTLPL-----
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44 PHOSPHOPANTETHEINE (BY SIMILARITY)
02. THIOESTERASE (BY SIMILARITY).
404079 MW; 6FD095704F858E6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                963;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN 1 (ADIPATE-ACTIVATING):
DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
PHOSPHOPANTETHEINE (BY SIMILARITY
PHOSPHOPANTETHEINE (BY SIMILARITY)
                                                                                                                                                                                                             InterPro; IFRO03030; Fpanueracatacan.
InterPro; IFRO01031; Thioesterase.
Peam, PE00501; AMP-Dinding; 3.
Peam, PE00550; Pp-binding; 3.
Peam, PF00550; Pp-binding; 3.
Peam, PF00550; Pp-binding; 3.
Peam, PF00550; Prosesterase; 1.
PENINTS; PR00154; AMPBINDING.
PROSITE: PS000154; PHOSPHOPANTETHEINE; 2.
PROSITE: PS000455; AMP_BINDING; 1.
PROSITE; PS00075; ACP_DOMAIN; 3.
PROSITE; PS0075; ACP_DOMAIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CYSTEINE-ACTIVATING).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1484.5; DB 1; Length
Pred. No. 2.7e-77;
4; Mismatches 1071; Indels
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 European Bioinformatics Institute.
                                                                                                                                                                                                    InterPro; IPR003880; Ppantne_attach.
                                                                                                                                                                                   Condensatn
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                                                                                                                        PIR; S18268; S18268.
HSSP; P14687; 1AMU.
InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensat
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                                                                                                        EMBL; X57310; CAA40561.1; -.
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InterPro; IPR003880; Ppantne_attach.
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InterPro; IPR001242; Condensat
                                                                           EMBL; X54853; CAA38631,1; -.
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HSSP; P14687; 1AMU.
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                        2932 GIDDDFFRCGGDSISALHLASQVQREIERKVSVKYLFDHPT-------VRSFVDNV 2980
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                                                                                                                                                                                                                                         3120 VWFALHHLVVDTVSWHILAQDLEILYNGGDLGAKTGSYRQWAQAVRDYTPAEGEREFWAE 3179
                                                                                                                                                                                                                                                                           ----NIITQATV 2945
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                    3180 TTRDMESAELLAQT----EGTTRRREEFALTAPDTRTLLAESPWAYDTEVNDLLLTATG 3234
                                                                                                                                                                                                                                                                                                                             2946 FNAACALVLSRESDSKDVVFGRIVSGR---QGLPVEYQDIVGPCTNAVPVRAHIESSDYN 3002
                                                                                      LSG--LAESSG-----DDEPEQGRLTGECPMLPIQE-----WFFAKPLADRHRWNHNFAIR
                                                               VGGREMAEYSPFQLLFTEDPEEFMASEIKPQLELQEIIQDIYPSTQMQKAFLFDHTTARP
                                                                                                                                                                                                 ----DDGTAR
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         GITDNFFDLGGHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEI
                                                                                                                 RPFVPFYIDFPSTSEPDAAGLIKACESLVNHLDIFRTVFAEASGELY---QVVLSCLDLP
                                                                                                                                                                     2793 IQVIETED------NINTATNEFLDEFAKEPVRLGHPLIRFTIIKQTKSMR
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Maccabe A.P., van Liempt H., Pallissa H., Unkles S.E., Riach M.B.R.,
Pfeifer E., von Doehren H., Kinghorn J.R.;
"Delta-(L-alpha-aminoadiyl)-L-vysteinyl-vvaline synthetase from
Aspergillus nidulans. Molecular characterization of the acvA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding the first enzyme of the penicillin biosynthetic pathway."; J. Biol. Chem. 266:12646-12654(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACV ARE ACTIVATED AS AMINOACYL-ADENYLATES WITH PEPTIDE BONDS FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER
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TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=5072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetase
                                                                                                                                                                                                                                                                          2895 VIQNTPMTILSDDTVVDGNDATCKALHLSKIVNIPSQVLRGSS--
                                                                                                                                                                                      ::: | : | : | 3078 VRGLADADLRQRLVDWQRTFDLANGPTACAAYLHGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine;
EC 6....) (ACY syntheraeu, News.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 YDVPTDIDISRFALAWKEIVNQTPALR-AFAFTSDSGKTSQVILKDSFVFSWMCW--SSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 ------DLNASVFP-----HLSDH------LAVPNPTTTAEHRITFPLSQKALSN 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 SSPDEVV-----RDEA----AAAASGPRCNRFVLLEDMQTK-KCQLVWTFSHALVDVTF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGALLVAYYDHNVI-DSLQTTR--LLQQFGHLIKCLQSPLDLSSMAEVNLMTEYDRAEIE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWNSQPLEVQDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLR 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          979 YDVNINPDL -- FKKAWKQVQHMLPTLRLRFQWGQD----VLQVIDEDQPLNWWFLHLADDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 QQRVLSRVFAAYKHEKDTHRPETPESSDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1089 LPLLFRKTHGTYLHLLHGHSLRTLE----DPYRQSQQYLQDHREDH----LRYWAGIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAICRTALSILLSRYTHSDEALFG-AVTEQSLPFDKHYLADGTYQTVAPLRVHCQSNLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1317 ELKYTIEGNIEKLDYPLAVIARE------VDLTGGFTFTICYAREL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRALLLHCQMES
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DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHOPANTETHEINE (BY SIMILARITY)
PHOSPHOPANTETHEINE (BY SIMILARITY)
PHOSPHRASE (BY SIMILARITY).
422448 MW; CB66B6D232A58CB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO00379; Ser_estrs_site.

R InterPro; IPRO00379; Ser_estrs_site.

R InterPro; IPRO01031; Thioesterase.

R Pfam; PF00550; pp-binding; 3.

R Pfam; PF00658; Condensation; 3.

R Pfam; PF00975; Thioesterase; 1.

R RINTS; PR00154; AMPBINDING; 3.

R PROSITE; PS000154; PHOSPHOPANTETHEINE; 3.

R PROSITE; PS000455; AMP_BINDING; 3.

R PROSITE; PS00075; ACP_DOMAIN; 3.

R PROSITE; PS0075; ACP_DOMAIN; 3.

R PROSITE; PS50075; ACP_DOMAIN; 3.

R PROSITE; PS50075; ACP_DOMAIN; 3.

R PROSITE; PS00075; ACP_DOMAIN; 3.

R PROSITE; PS00075; ACP_DOMAIN; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 444; Mismatches 1025; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1422.5; DB Pred. No. 1.2e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479
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	2686 3113	2746 31 <sup>3</sup> 5	2800 3194	2857 3250	290 <b>2</b> 3309	
2579 QPVSDGQQQDRSAHMAPRTETEAILCDEFAKVLGFQ-VGITDNFFDLGGHSLMATKLAVR 2637   2579GNPQHQISYNPPRDVLEADLCRLWASALGTERCGIDDDLFRLGGDSITALHLAAQ 3059	IGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAEYSP    ::  : :      :	FOLLFTEDPEEFMASEIKPQLELQEILQDIYPSTOMQKAFLFDHTTARPRPFVDFYIDFP   :     :	STSEPDAAGLIKACESLVNHLDIFRTVFAEASGELYQVVLSCLDLPIQVIETED	-NINTATNEFLDEFAKEPVRLGHPLIRFTIIKQTKSMRVIMRISHALYDGLSLEHVVR  : : :     : :     : :     : :     : :       : :       : :	2858 KLHMLYNGRSLLPPHOFSRYMQYTADGRESGHGFWRDVIQNTPMT 	2903ILSDDTVVDGNDATCKALHLSKIVNIPSQVLRGSSNIIT 2941       :
3005	3060	3114	2747 3136	3195	325	3310
Qy Dp	Qy Dp	Qy	Qy	Qy Db	. YO	Qy

Search completed: May 30, 2003, 12:46:02 Job time: 139 secs



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OM protein - protein search, using sw model

Run on:

May 30, 2003, 12:40:46; Search time 78 Seconds (without alignments) 3856.469 Million cell updates/sec

US-09-482-788-2 16128 1 MEYLTAVDGRQDLPPTPASF.....RVEHLLEEVSKTFEGLNSSL 3129 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% . Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	enniatin synthetas	cyclosporin synthe	pristinamycin I sy	tyrocidine synthet	virginiamycin S sy	bacitracin synthet	gramicidin S synth	CDA peptide synthe		. bacitracin synthet	syringomycin synth	probable non-ribos	tyrocidine synthet		peptide synthetase	surfactin syntheta		synt	gramicidin S synth	mycosubtilin synth	peptide synthetase	. bacitracin synthet	pyoverdine synthet	$^{\circ}$	actinomycin synthe	HC-toxin synthetas	hypothetical prote	CDA peptide synthe	peptide synthetase
SUMMARIES	ID	539842	S41309 .	T30289	T31076	T30874	T31679	JX0340	T36249	AI2136	T31677	T14593	F83345	T31075	T36248	C69681	I40486	AE2136	I40457	YGBSG2	T44807	D69681	T31678	5399	H83343	T14591	A45086	E98274	618	140456
	DB	8	N	7	~	~	7	7	7	7	7	7	~	~	7	7	~	7	-	П	7	Н	7	7	~	7	~	7	7	-
	Length	(7)	15281	4848	6486	1997	6329	4450	3670	2588	5255	9376	5149	3587	7463	2555	3587	2617	2560	4452	5369	3603	2607	2448	4342	2611	5232	2566	2117	2561
œ	Query	60.3	31.0	14.1	12.9	12.3	12.2	12.0	11.8	11.8	11.7	11.6	11.6	11.3	11.2	11.2	11.1	11.0	11.0	10.9	10.7	10.7	10.6	10.6	10.4	10.4	10.1	10.0	10.0	6.6
	Score	9720	2000	2275.5	2084	1984	1975	1933	1906.5	1896.5	1882.5	1876.5	1867.5	1816	1810	w	1793.5	1781.5	1769.5	1758	1729.5	1725	1710	1708.5	1677	1672	625	1612.5	611	1604
	Result No.		7	m	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	. 20	21	22	23	24	25	36	27	28	29

61 DCNALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPALRAFAFTSDSGKTSQVILKD 120 

QY Ω

q

surfactin syntheta	peptide synthetase	peptide synthetase	alpha-aminoadipyl-	pristinamycin I sy	delta-(L-alpha-ami	enniatin synthetas	delta-(L-alpha-ami	hypothetical prote	probable peptide s	probable non-ribos	saframycin Mx1 syn	hypothetical prote	alpha-aminoadipyl-	alpha-aminoadipyl-	lysobactin synthet
140485	T14165	AI3009	YGCEVC	T30288	S18268	S53111	A40889	G89779	T30192	B83346	T18552	T17484	YGPLV8	YGPLV3	T18545
7	7	7	Н	7	٦	7	7	7	7	~	~	~	Н	Н	7
3588	4976	2157	3712	2591	3649	492	3770	2391	10797	1317	2605	4077	3791	3746	1575
6.6	9.5	9.5	9.4	9.5	9.5	0.6	8.8	8.7	8.6	9.8	8.5	8.4	8.4	8.3	8.3
1601	1538.5	1532	1515	1491	1484.5	1453.5	1422.5	1402	1391.5	1387	1366.5	1358	1347.5	1346.5	1331
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

· · · · · · · · · · · · · · · · · · ·	RESULT 1 S19842 cnitatin synthetase - fungus (Fusarium scirpi) Cpacies: Rusarium scirpi C;Species: Rusarium scirpi R;Haese, A. summitted to the EMBL Data Library, November 1992 R;Haese, A. A;Reference number: S19842 A;References: BMBL:1218755; NID:92729; PIDN:CAA79245.1; PID:92730 A;Residues: 1-3131 <hae> A;Residues: 1-3131 <hae> A;Residues: 1-3131 <hae> A;Residues: 1-3131 <hae> A;Reference number: S19906; MUID:93247491; PMID:8483420 A;Title: Molecular characterization of the enniatin synthetase gene encoding a multif A;Reference number: S19906; MUID:93247491; PMID:8483420 A;Accession: S19906 A;Accession: S19906 A;Accession: S19906 A;Accession: S19906 A;Accession: S63363 A;Attle: Arrangement of catalytic sites in the multifunctional enzyme enniatin synthe A;Reference number: S53563; MUID:95324513; PMID:7601090 A;Accession: S63363 A;Molecule type: protein A;Reference number: S63363 A;Molecule type: protein A;Reference number: S63363 A;Reference number:</hae></hae></hae></hae>
	F;1603-2100/Domain: acetate-CoA Íigase homoľogy <acl2> F;2507-2574/Domain: acyl carrier protein homology <acp1> F;2601-2667/Domain: acyl carrier protein homology <acp2> F;1047,2538,2632/Binding site: phosphopantetheine (Ser) (covalent) #status predicted</acp2></acp1></acl2>
	Ouery Match 60.3%; Score 9720; DB 2; Length 3131; Best Local Similarity 60.8%; Pred. No. 0; Matches 1939; Conservative 443; Mismatches 691; Indels 114; Gaps 32;
	Qy 1 MEYLTAVDGRODLPPTPASFCSHGDSPLNSSYBQLFHLYGLDSSRIBAIKPCTPFOLDMI 60

1185 MKVIDLCGSDLDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHILLITWHHIISDGWS ::	1423 1417 1483 1543 1603	1597 1663 1657 1723 1712	1783 1772 1843 1831 1903 1890	0 0 0 0 0	
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QY         121 SFVFSWMCWSSSSSPDEVVRDEAAAAASGPRCNRFVLLEDMQTKKCQLVWTFSHALVDVT 180           11   1   1   1   1   1   1   1   1   1	IGHLAPPECLRDIRNTGDNGSAACDFGTVLLVTDGSHVNNGINGFLQGTESS  GARACLENIASAGDDSAACGSRPFSWSQMETPSQHLLGKFSRKTEFF  NRALLLHCQMESSGALLVAYYDHNVIDSLGTRLLQGFGHLIKCLQSPLDLSSM	529 AVHIKSLGLRAQOAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVYTOTR 588  1	DRMNSIPSFINRYNVNHMMATPSYMGTFSPEDVPGLATLVLVGEQMSSSVNAIWAPKLQL 76	QVKIRGQRVELGAIETHLRQQMPDDLTIVVEATKRSQSANSTSLIAFLIGSSYFGNRPSD	1066 RSVGMDLKVSNIYOPPTLAGISAVVKGPLZYTLIPKSTHEGPV-EQSYSGGKLWFLDDL 1124

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1993

PID:g440169 Library, November

acetate-CoA ligase homology

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EHRGIT------RLVKNSNVVAKQPAAAAIAHLSNIAFDASSWEIYAPLLNGGTVVCI 11806
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| 11865 AILARRAVGSGVYNAYGPTENTVLSTIHNIGENEAFSNGVPIGNAVSNSGAFVMDQN--Q 11922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIPSDDDRMNSIPSFINRYNVWWMMATPSYMG---TFSPEDVPGLATLVLVGEQMSSSVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 AIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQT--RATVALTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;14698-14765/Domain: acyl carrier protein homology <AC11>F;1060,2558,4045,5537,7034,8094,9589,11086,12158,13654,14729/Binding
                        A,Accession: $45487
A;Status: nucleic acid sequence not shown
A;Molecule type: DA
A;Residues: 1-15281 <WEB>
A;Residues: 1-15281 <WEB>
A;Rocos-references: EMBL:228383; NID:9440168; PIDN:CAA82227.1; PID:97 Note: the nucleotide sequence was submitted to the EMBL Data Libra A;Note: the nucleotide sequence was submitted to the EMBL Data Libra A;Note: the source is designated as Tolypocladium inflatum C;Genetics:
A;Genetic code: SGC3
C;Superfamily: cyclosporin fungus cyclosporin synthetase; acetate-CG C;Keywords: carrier protein; phosphopantetheine; phosphoprotein F;532-1008/Pomain: acetate-COA ligase homology AGCLL>
F;1029-1066/Pomain: acyl carrier protein homology AGCLL>
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       PMID:8001164
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number: S45487; MUID:95094306; S45487
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C;Species: Tolypocladium inflatum (cyclosporin fungus)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Nov-2000
C;Accession. 345487; S4130
R;Weber, G.; Schoergendorfer, K.; Schneider-Scherzer, E.; Leitner, E.
Curr. Genet. 26, 120-125, 1994
A;Title: The peptide synthetase catalyzing cyclosporine production in Tolypocladium nive
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13057 2018 13116		DD 13235 FPSLAGSARVHVGTAEDISSIDGLR QY 2196 FFGDVRSQATNEHFLAARAIHTLGK	Qy 2256 PGLVEHVEILPKNMEAVNELSAYRY,    ::	Qy 2358 STIRSSABGDSSLSVPDIFRIAGEAC   :   :    :     Db 13474 SRTQSRAKECPALSVADLIEIGKGIO   Qy 2412 RTLVNFPTDHHLRGSDLITNRPLQRI   :	13531 2472 13591	Qy 2532 GGHSLLATKLISRIDORLKVRITVKI 	1371 257 .	Oy 2575	13 2 13	Db 14011 TESLVOQVRSTTATAFENQDVPFBF	57
923SANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVL 965 12029 PELVAFFSLKGNAGTNGVNGVSDQEKIDGDEQHALLMENKIRHNLQALL 12078 966 PRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQTOGAIVQQAPAPIPVFADTAA 1025   :	1026 KLHSIWVQSLGIDPATVNVGATFFELGGNSITAIKM-VNMARSVGMDLKVSNIYQH 1080	12185 PVVGQLAASIQOGSTPHEAIPALSHSGPVQQSFAGGRLWFLDRFHINAAWTIMPEGVRLR 12244 1141 GPVNVDALRRALAALEQRHETLRTFEDQDGGVQIVHEKLSEBMKVIDLCGSDLDPFEV 1200		1378 1248 1438		1499 SVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHV- 1557  1	12663 PDFATEASVUDVEQUANDEDLANDESCRIPTION SECUNDARIAN 10:10  12663 PDFATEASVUDVEQTQVVANPDALAVIDISTKLTYAELDQQSDHVAAMLSKQKLPAESIV 12722  1617 AVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDI 1676  1	1677 EVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVI 1736 :		1852VQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGRALN-NSGAYVVD 1897 :	1898 PEQQLVGIGVMGELVVTGDGLARGYSDKALDENRFVHITVNDQTVKAYRTGDRVRXRIGD 1957 1111
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HPDLVVLNSVIQYFPSSEYLAEIADTLIHLPNVQRI 2195 MYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHE 2077 RDDDAYLEPLQKEQQTPFDLASEPGWRVALLKLGKD 13830 LGQFYLAAKSGKAPLSQVAPLPIQYRDFAVWQRQEE 13890 LADYTRPNVLSGEAGSVSFVINDSVYKSLVSFCRSR 13950 SSGMILFNLD--SRLESYVGLEPSRSAAAFVNKATES 2135 KNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRF 2255 VSKIPFEITAFERQVVASLNSNID-----EWQL 2357 FALRMRGPLQVDALAAALVALEERHESLRTTFEERD 13770 ATIGTPIANRNRPELENLIGCFVNTQCMRITIGDDE 14010 AGFRVEVSSARQWSQNGALDAVFH-----HCCSQG 2411 SRIVSTLSAGSRDTSRNPLVQLLFAVHSQQGLGRIQ 14070 DEADRLNGSVMFATDLFQPETIQGFVAVVEEVLQRG 14130 APLPTFPISEVEVILCEEATEVFGMKVDITDHFFNL 2531 KDVFDHPVFADLASVIRQG------ 2574 2574 222 97-----TG 5224

qq	14131 LEOPOSPIATMPLAEGIAQLRDAGALQMPKSDYPRNASLVDVFQQQAMASPSTVAVTDST 14190	
Qy	2583 2582	3103 TQLFGRRVEHLLEEVSKTFEGLN 3126  :
QQ	14191 SKLTYAELDRLSDQAASYLRRQQLPAETWVAVLAPRSCETIIAFLAILKANLAYMPLDVN 14250	Db 15256 RQILGEKVVGSMLNELCETMLALS 15279
Qy	2583 2582	RESULT 3
qa	14251 TPSARMEAIISSVPGRRLILVGSGVRHADINVPNAKTMLISDTVTGTDAIGTPEPLVVRP 14310	T30289 pristinamycin I synthase 3 - Streptomyces pristinaespiralis
QY	2583 2582	<pre>C;Species: Streptomyces pristinaespiralis C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000</pre>
qq	14311 SATSLAYVIFTSGSTGKPKGVMVEHRAIMRLVKDSNVVTHMPPATRMAHVTNIAFDVSLF 14370	C.Accession: T30289 Rich Creev-Lagard, V.A.; Saurin, W.; Thibaut, D.; Gil, P.; Naudin, L.; Crouzet, J.; B
Qy	2583 2582	Submitted to the EMBL Data Library, February 1997 A Description: Streptogramin B biosynthesis in Streptomyces pristinaespiralis and Str
οp	14371 EMCATLLNGGTLVCIDYLTLLDSTMLRETFEREQVRAAIFPPALLRQCLVNMPDAIGMLE 14430	A; Kererence number: Z20808 A; Accession: T30289 A.ctatus: prodiminary: translated from Co/publ/Anbi
Qy	2583 2582	A; Scarus: pretinition y; translated from ob/EmbL/DDBJ A; Molecule type: DNA
QQ	14431 AVYVAGDRFHSRDARATQALAGRRVYNAYGPTENAILSTIYNIDKHDPYVNGVPIGSAVS 14490	A; Residues: 1-4646 < DEC> A; Residues: 1-4646 < DEC> A; Cross-references: EMBL:Y11548; NID:e1025755; PID:e307539; PIDN:CAA72312.1
Qy	2583 2587	Cigenetics: Aigene: SnDDE Cinnarfamily: and carrier protein homology: acetata=CoA linasa homology
qa	14491 NSGAYYMDRNQQLLPPGVMGELVVTGEGVARGYTDASLDTDRFVTVTIDGQRQRAYRTGD 14550	acy, cantie, process nomotopy, accede con rigase rier protein; phosphopantetheine; phosphoprotein
δλ	2588 2587	in: acyl carrier protein homology <acpi></acpi>
qq	14551 RVRYRPKGFQIEFFGRLDQQAKIRGHRVELGEVEHALLSENSVTDAAVVLRTMEEEDPQL 14610	F:1209-1204/Domain: acetate-CoA iigase homology #status atypical <aclz> F:2399-2467/Domain: acyl carrier protein homology <acpz></acpz></aclz>
ογ	2588 2587	ain: ain:
QQ	14611 VAFVTTDHEYRSGSSNEEEDPYATQAAGDMRKRLRSLLPYYMVPSRVTILRQMPLNANGK 14670	043-4492/Jomain: acetate-coa iigase homology <acl4> 507-4575/Domain: acyl carrier protein homology <acp4></acp4></acl4>
, Qy	2588 -DRSAHMAPRTETEAILCDEFAKVLGFQVGITDNFFDLGGHSL 2629	;998,2431,3475/binding Site: phosphopantetheine (Ser) (
Db		atch 14.1%; Score 2275.5; DB 2; Length 4848; cal Similarity 26.7%; Pred. No. 9.8e-124;
Oy	2630 MATKLAVRIGHRLDTTVSVKDVFDHPVLFOLAIALDNLVQSKTNBIVGGREMAE 2683	Matches 877; Conservative 474; Mismatches 1280; Indels 659; Gaps
QQ	14731 LATKLAARLSRRMGLRISVKDLFDDPVPVSLAGKLEQQQGFSGEDESSTVGIV 14783	/Z GHAVIDVPIDIDISKFALAWKELVNQYFALKAFAFTSDSGKTSQVILKDSFV
Qy	2684 YSPFQLLFTEDPEEFMASEIKPQLEL-QEIIQDIYPSTQMQKAFLFDHTTARPRPFVPFY 2742	31 GPDVITVQMVFELRGPLDEDGLRAAAAALLKRHPNLKAGFWQQGVERFVQFV
qa		124 FSWMCWSSSSPDEVVRDEAAAAS
. Qy	2743 IDFPSTSEPDAAGLIKACESLVNHLDIFRTVFABASGELYQVVLSCLDLPIQVIETEDNI 2802	83PNEVPLPWHIRDFTALGESDRERAVEATVTADRAEREDPGAPPLIREAL
Db	:     :	158 LEDMQTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPESSDATDTDS :: :
Qy	2803 NTATNEFLDEFAKEPVRLGHPLIRFTIIKQT-KSMRVIMRISHALYDGLSLEHVVRKLHM 2861	132 L-GLAADHHKLVLTTHHLLLDGWSMPLLVKELFTLYGQRGDDAGMPPVTFYKAYLAHLAG
qq	: :::    ::	SSVSVSMS :
Οy	2862 LYNGRSLLPPHQFSRYMQYTADGRESGHGFWRDVIQNTPWTILSDDT-VVDGNDATCKAL 2920	262 TTAEHRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFGAVTEQ-
qq	14960 LYSDKHLAQAPKFGLYMHHMASRRAEGYNFWRSILQGSSMTSLKRSVGALEAMTPSAGTW 15019	240 TTAGLTALARSCNITLOHPGAKRLGTAARPOLGRDDVVFGATVAHR
yo q	HLSKIVNIPSQVLRGSSNIITQATVFNAACALVLSRESDSKDVVFGRIVSGRQGLPVEYQ	SLPFDKHY
an i	QISKSIRIPPAALKNGITQATLFTAAVSLLLAKHTKSTDVVFGRVVSGRQDLSINCQ	Db 286 PPEIPGIESTIGMFINTLPVRVRVRPAETLGDLIGRVQREQAALIEHRHLSLTDIRST 343
<i>5</i> €	2981 DIVGPCTRAVPVRAHI ESSDYNDILHDIODOYLLSLPHFTIGFSDLKRNTTDWPEAITN 3039	Qy 367 GDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRALLLHC 417
ò		-PLSLLA
7 do		418 QMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVN
Qy	IAGEV	394PGESLRFRLDHRGDVLDEAGARLLLERLDTLLTDIAEHGADLPVGRLDLLSAAERH
QO	15197 NGTNGTHANGINGSNGVNGRDSNVVSAAGDQAPVHDLDIVGIPEPDGS-VKIGIGAS 15255	Qy 468 LMTEYDRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSR 527 :  :    :    :  ::    :    :

qa .	450 QVLEEFNDTGLPAEDATLAALFEAQAARTPDTTALLVGGRSLTYAELNARANR 502	ě	
Qy	528 LAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQT 587	δŌ	
qa	503 LARHLVTLGAGPEQ-IVAVKLERSLDLYVALLAVLKTGAAYLPVDTAYPAERIAFMMDDA 561	o O	
Qy	588 RATVALTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTKSQDLAYVIFTS 642	oy 1	1598 SDIL
qa	562 RPAVVLTGEDTGQDLSGYDDTDLTDADRTAPLLPAHPAYVLTTS 605	an d	
οy	643 GSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCV 702	λo :	
qq	606 GSTGTPKAVVMPGAALVNLLAWHRREIPGEAGAPVAQFTTIGFDVAAQEILATWLHGKTL 665	QQ ·	
Oy	703 CIPSDDDRMNSIPSFINRYNVNWMMATPSYMGTFSPEDVPGLATLVLVGEQM 754	οy	1717 LYTS
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Qy	755 SSSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRAV-GAHSWV 803	Óγ	1776 GRTL
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QY	804 IDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDG 859	ΟŅ	1835 TDST/
qq	:  :  :      :	qq	1768 GDAT
Oy	860 AKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIVVEA 917	δλ	
qa	::         : :   :	QQ	
ΔO	918 TKRSOSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEOVI.PRHSIPSFVICM 977	QY	1949 DRVR
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Qy	1036 GIDPATVNVGATFFELGGNSITAIKMVNMARSV-GMDLKVSNIYQHPTLAGISAVVKGDP 1094	7 E	
qq	986 GIDDGER 1033	ì	
QY	1095 LSYTLIPKSTHEGPVEQSYSQGRLWFLDQLDVGSLWYLIPYAVRWRGPVNVDAL 1148	ò d	
qa	1034 IDQASGARPALTPAERPE-RLPLSHAQRRLWFLGRLDGPNSTYNIPLALRLSGTLDTAAL 1092	on o	VASA TCOZ
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<b>q</b>	1432 DLGLAVIEEHTADGTRAGIRGDWEYSTELFERGTVEALGSRLVRLLDAVADDPERTIGSV 1491		

GPTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATS-LAYV 1716 RPALVV---DAIPDDTTLAAYADSRLTDA------DRSAPLLPAHPAYV 1653 ||||| ||||: || : || : || : || SGSTGAPKGLGTHSRVLNFASISFDAAVWELTSALFT 1713 IDFDEMHEWLGETTRTLHDNRSLG----NVLEIGTGSGMILFNLDSRLESYVGLEPS 2122 AAFVNKATESIPSLAGKAKVQVGTATDIGQVDDLHP---DLVVLNSVIQYFPSSEYL 2179 LHRAAELLAPG-GTIFLGDIRNLRTLHAFRTAVELRRAGPFADPAAVRRAVEQSLAT 2166 DGIVTLEKLDVENVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQ 1597 LAGWLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILS 1657 SGSTGRPKGVMIEHRVIIRTVTSGCIP-NYPSETRMAHMATIAFDGASYEIYSALLF 1775 LVLADADDLLPGPSLARLVHDRHITLIALPPSALPALPDGALPPGTD-----LIVA 1767 TAPDALDAGGLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGV-PIGRALNNSGA 1893 RYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPE 2008 FVVAD-HDHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPS-TIGSDFKGWTSMYD 2066 DDWIDFQANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAFERQVVASLNSNIDEWQL 2357 ETVLRWGT------DLDTAGELARVLSGPRPVRVTGIPN---ARLTGETRAAQA 2267 RSSAEGDSSLSVP-----DIFRIAGEAGFRVEVSSARQWSQNGALDAVFHHCC 2408 ----RTLVNFPTDHHLRGSDLLTNRPLQRLQNRRIAIEVRERLRSLLPSYMIPSNI 2463 DKMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCEEATEVFGMKVD 2523 LVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVP-LRVPRRLSRTLMFFFLVV 1834 ADTLIHL--PNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDM 2237 LLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLP 2297 TAYRPRIGROGP-----LANDPARAEQDAALVGELRDLVAQRLPAHMAPAAY 2364 HFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIRQGLGLQQPVSD 2583 | ::||::|||:|| | DRLPLSANGKLDR-------DALPAP-----

F;6165-6233/Domain: acyl carrier protein homology <acheeolery #st="" 136;="" 1372;="" 2.9e-112;="" 23.0%;="" 46="" 595;="" 864;="" 928;="" <acheeolery="" best="" carrier="" conservative="" covalent)="" gaps="" homology="" ieaikpctpfqldmidcnaldkqsaighavd<="" indels="" local="" match="" matches="" mismatches="" no.="" pred:="" protein="" query="" qy="" similarity="" th=""><th>OY 153 NRFVLLEDMOTKKCQLVWTFSHALVDVTFQQRVLSRVFAAXKHEKDTHRPE 203  113 HAPDLTKDNLMKAAIFQTAENKYRLVWAFHHIVDGWTLGVLLHKLLTYYAALRKG 168  OY 204 TPESSDATDTDSQSVSVSMSCEDNAVSATHFWQTHLNDLNASVFPH 250  169 EPIPREATKPYSEYIKMLDKQNKDEALAYWQNYLAGYPHQAAFPKKLGTEASRYEH 225  OY 251 LSDHLMVPNTTTAEHRITFPLSQKALSNSALCRTALSILLSRYTHSDEALFGAVTEQSL 310  1</th><th>363 IRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQOITESSHFM</th><th>A 85 CGEDILITOELMERSAQLANALREKGI-ASGSIVSIMAEHSLELIVAIMAVLKSGAATLP 343  QY 571 IDPNDPPARTAQVYQTRATVALTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLT 630   </th><th>QY         748 VLVGEQMSSSVNAIMAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRA 796           DD         717 IRRFIVGGENLPTKLAKQIYDHFGENVQIFNEXGPTETVVGCMIYLYDPQTTTQESVPIG 776           QY         797 VGAHSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPA 853           I         1 :: 1 : 1 : 1   1   1   1   1   1   1  </th></acheeolery>	OY 153 NRFVLLEDMOTKKCQLVWTFSHALVDVTFQQRVLSRVFAAXKHEKDTHRPE 203  113 HAPDLTKDNLMKAAIFQTAENKYRLVWAFHHIVDGWTLGVLLHKLLTYYAALRKG 168  OY 204 TPESSDATDTDSQSVSVSMSCEDNAVSATHFWQTHLNDLNASVFPH 250  169 EPIPREATKPYSEYIKMLDKQNKDEALAYWQNYLAGYPHQAAFPKKLGTEASRYEH 225  OY 251 LSDHLMVPNTTTAEHRITFPLSQKALSNSALCRTALSILLSRYTHSDEALFGAVTEQSL 310  1	363 IRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQOITESSHFM	A 85 CGEDILITOELMERSAQLANALREKGI-ASGSIVSIMAEHSLELIVAIMAVLKSGAATLP 343  QY 571 IDPNDPPARTAQVYQTRATVALTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLT 630	QY         748 VLVGEQMSSSVNAIMAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRA 796           DD         717 IRRFIVGGENLPTKLAKQIYDHFGENVQIFNEXGPTETVVGCMIYLYDPQTTTQESVPIG 776           QY         797 VGAHSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPA 853           I         1 :: 1 : 1 : 1   1   1   1   1   1   1
	2552 2816 2868 2868 2642 2904 2702 2752	OY 3023 FSDLKRNCTDWPEAITNFSCCITYHNFEXHPESQFEQQRVEMGVLTKFVNIE 3074	C; Date: 0.2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000 C; Date: 0.2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000 C; Accession: 71076 #s. Marahiel, M.A. J. Bacteriol. 179, 6843-8850, 1995 A; Hitle: The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequ. A; Reference number: 220969; MuID: 98012987; PMID: 9352938 A; Accession: T31076 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href="Molecule type: DNA">Molecule type: DNA</a> A; Residues: 1-6486 <a href<="" td=""><td>G.Function:  G.Function:  G.Function:  C.Superfamily: acyl carrier protein homology; acetate-CoA ligase homology C.Superfamily: acyl carrier protein homology; acetate-CoA ligase homology G.Keywords: carrier protein; phosphopantetheine; phosphoprotein C.Keywords: carrier protein homology <acli> F.510-950/Domain: acetate-CoA ligase homology <acli> F.156-1036/Domain: acetate-CoA ligase homology <acli> F.1505-2073/Domain: acetate-CoA ligase homology <acli> F.2583-3025/Domain: acetate-CoA ligase homology <aclia> F.3613-106/Domain: acetate-CoA ligase homology <aclia> F.3621-406/Domain: acetate-CoA ligase homology <aclia> F.4078-4146/Domain: acetate-CoA ligase homology <aclia> F.4056-5104/Domain: acyl carrier protein homology <aclia> F.4056-5104/Domain: acyl carrier protein homology <aclia> F.5122-5190/Domain: acetate-CoA ligase homology <aclia> F.5122-5190/Domain: acetate-CoA ligase homology <aclia> F.5122-5190/Domain: acetate-CoA ligase homology <aclia> F.5702-6147/Domain: acetate-CoA ligase homology <aclia< td=""></aclia<></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></acli></acli></acli></acli></td></a>	G.Function:  G.Function:  G.Function:  C.Superfamily: acyl carrier protein homology; acetate-CoA ligase homology C.Superfamily: acyl carrier protein homology; acetate-CoA ligase homology G.Keywords: carrier protein; phosphopantetheine; phosphoprotein C.Keywords: carrier protein homology <acli> F.510-950/Domain: acetate-CoA ligase homology <acli> F.156-1036/Domain: acetate-CoA ligase homology <acli> F.1505-2073/Domain: acetate-CoA ligase homology <acli> F.2583-3025/Domain: acetate-CoA ligase homology <aclia> F.3613-106/Domain: acetate-CoA ligase homology <aclia> F.3621-406/Domain: acetate-CoA ligase homology <aclia> F.4078-4146/Domain: acetate-CoA ligase homology <aclia> F.4056-5104/Domain: acyl carrier protein homology <aclia> F.4056-5104/Domain: acyl carrier protein homology <aclia> F.5122-5190/Domain: acetate-CoA ligase homology <aclia> F.5122-5190/Domain: acetate-CoA ligase homology <aclia> F.5122-5190/Domain: acetate-CoA ligase homology <aclia> F.5702-6147/Domain: acetate-CoA ligase homology <aclia< td=""></aclia<></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></aclia></acli></acli></acli></acli>

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OY 2567 LASVIRQCLGLQOPVSDGQGQDRSAHMAPRTETEAILCDEFAKVLGFQ-VGITDNFFD 2623	2624 LGGHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAE 1	OKAELEDHTTARPRPE 		OY 2798 TEDNINTATNEFLDEFAKEPVRLGHPLIRFTIIK-QTKSMRVIMRISHALYDGLSLEHVV 2856					DEPLYDLAIAGEVEPDGAGLKVTVIAKTQLFGRKRVEHL 3114   :    :    :    :    :    :    :    :	RESULT 5	rginiamycin S synthetase - Streptomyces virginiae (fragment) Species: Streptomyces virginiae Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 01-Dec-2000 Accession: 710R74	de Crecy-Lagard, V.A.; Saurin, W.; Thibaut, D.; Gil, P.; Naudin, L.; Crouzet, J bmitted to the EMBL Data Library, February 1997 Description: Streptogramin B biosynthesis in Streptomyces pristinaespiralis and Reference number: 220808	Accession: T30874 Status: preliminary; translated from GB/EMBL/DDBJ Wolecule type: DNA Residues: 1-1997 < PRC>	Cross-references: EMBL:Y11547; NID:e1025754; PID:e307537; PIDN:CAA72310.1 Genetics: Generics: SabbB Superfamily: Acetato-Coa lines homology: Acetato-Coa lines homology:	C; Keywords: carrier protein; phosphopantetheine; phosphoprotein nomology (; Keywords: carrier protein; phosphopantetheine; phosphoprotein F;113-553/Domain: acetate-CoA ligase homology <acl> F;568-636/Domain: acyl carrier protein homology <acn> F;600/Binding site: phosphopantetheine (Ser) (covalent) #status predicted</acn></acl>	Query Match 12.3%; Score 1984; DB 2; Length 1997; Best Local Similarity 29.2%; Pred. No. 2.5e-107; Matches 618; Conservative 378; Mismatches 899; Indels 222; Gaps 66;	431 DHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEYDRAE-IESWNSQPLEV 4	488 QDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVY

R;Konz, D.; Klens, A.; Schorgendorfer, K.; Marahiel, M.A.
Chem. Biol. 4, 927-937, 1997
A;Title: The bacitracin biosynthesis operon of Bacillus licheniformis ATCC 10716: mol
A;Reference number: 221058; MUID:98089193; PMID:9427658
A;Ccession: T31679
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule:type: DNA

A; Cross-references: EMBL: AF007865; NID: 94464275; PID: 92982196; PIDN: AAC06348.1 C; Genetics:

A;Gene: bacC S.Superfamily: acetate-CoA ligase homology; acyl carrier protein homology C;Keywords: carrier protein; phosphopantetheine; phosphoprotein F;505-946/Domain: acetate-CoA ligase homology <ACLL>

F)964-1032/Domain: acyl carrier protein homology <ACPI>
F)1540-1978/Domain: acyl carrier protein homology <ACPI>
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F)1996-2063/Domain: acyl carrier protein homology <ACPI>
F)3046-3483/Domain: acyl carrier protein homology <ACI3>
F)3500-3568/Domain: acyl carrier protein homology <ACI4>
F)4526/Domain: acyl carrier protein homology <ACI4>
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F)559-6032/Domain: acyl carrier protein homology <ACI5>
F)560-6118/Domain: acyl carrier protein homology <ACI5>
F)533-7Binding site: phosphopantetheine (Ser) (covalent) #status predicted

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1925
VAADPDQPIGRVGILD---PAERHRILHTWN-DTSRPGADATWPELFQARAAEHPDAVAL 1136
                                                                                            LDVRSPSARVQDILSGLSGPTIVLIGHDTA----PPDIEVTNVEFVRIRDALNDSNADGFE 1699
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                           VIEHDSTKP-SATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIP----NYPSETR
                                                                                                                                                                        MAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALKDVFFREHVN-----AASHV
                                                                                                                                                                                                                                   1366 VLADDALPAGVD------LVVAGEATSPDQVGRWS--TGRRWINAYGPTEAAVCTT
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PALRAFAFTSDSGKTSQVILKDSFV-FSWMCWSSSSSPDEVVRDEAAAAASGPRCNRFVL 157

3 TKVEKIYPLSNMQKGMLFHAMKDEAS---HAYFEQFIIELKGDVDERMFEESLNEVMKRH

44 SRIEAIKPCTPFOLDMIDCNALDKOSAIGHA-----VYDVPTDIDISRFALAWKEIVNQT

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Length 6359; Indels

Query Match 12.2%; Score 1975; DB 2; L Best Local Similarity 24.3%; Pred. No. 7.1e-106; Matches 817; Conservative 599; Mismatches 1275;

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DIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESS-----HFMPCNNRALLL 415
                                                                                                                                                                                                                                                                       QSLPFDKHYLADGTYQTVAPLRVHCQSNLRASDVM-----DAISSYDDRLGHLAPF-GLR 361
                                                                                                                                                                                                               RDAEVEGIETMVGVFINTIPTRIRLDKDKLFKDVLRQTQADALESSRYNYMNLAEVQALS 336
                                                                                                                                                                                                                                                                                                                                                ----SISAALDDQLKLLFIYDENVYD---TTIIETLEKHIITVAEQVAEDETQTLRDINL 435
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                                                                                                                                    GFKRREKTIECS-KELTNRLIKLANRNHVTINTVLQSIWGVILAKYNNSEDVVFGTVVSG
                                                                                                                                                                                                                                                                                                                  HCQMESSGAL ---- LVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPL -- DLSSMAEVNL
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C;Species: Bacillus licheniformis
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000
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C; Accession: T31679

RESULT 6

T31679

67 KOSAIGHAVYDVPTDIDISRFALAWKEIVNOTPALRAFAFTSDSGKTS11			LMRVA	164 KKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPESSDATDTDSQSVSVV 221	135 GKVNYQMIMSFHHILMDGWCFNIIFNIYLSLKEKKPLQLEAVQPYKQFIKWL 190	SMSCEDNAVSATHFWQTHLNDLNASVFPHLSDHLMVPNPTTTAEHRITFP	EKQDKQEALRYWKEHLMNYDQSVTLPKKKAAINNTTYEPAQFRFAFDKVLTQQLL	2/2 LEQNALDNASALCKTALLESKTTHSDEARFGAVTEQSLPFDKHYLADGTYQTVAP 32/ 2/4	LRVHCQSNLRASDVMDAISSYDDRLGHLAPFGLRDIRNTGDNGSAACDFQTVL		381 LVTDGSHVNNGINGFLQQITESSHFMPCNNRALLLHCQMESSGALLVAYYDHN 433	362 LVEELQKNSIMQKVGFTVRDVKMFEPTNYDMTVMVLPRDEISVRLDYNAAVYDID 416	VIDSLQTTRLLQQFGHLIKCL-QSPLDLSSMAEVNLMTEYDRAE-IESWNSQPLEVQ     ::     ::   ::       ::	FIRKIEGHMKEVALCVANNPHVLVQDVPLLTKQEKQHLLVELHDSITEYP	489 DILLHHEMLAAVSHSPIKTALQAWDGDWTISELDNVSSKLAVHIKSLGLKAQQALIPVYF 548  487 DKWTHOLEPROVERDENVANTEREKVAVDET HEDGORATADE DERKAVATERETTILL 1	EXSKWVIASMLAVLKSGNAFTLIDPNDPPARTAOVVTOTRATVALTSKLHRETVOKLVGR			: ::  :   :   : : : : : : : : : : : : :	669 LGINSDTRALQFGTHAFGACLLEIMTLINGG-CVCIPSDDDR-MNSIPSFINRYNVWM 726	642 TNINFSDKVLQYTTCSFDVCYQEIFSTLLSGGQLXLIRKETQRDVEQLFDLVKRENIE-V 700	727 MATPSYMGTESPEDVPGLATLVLVGEQMSSSVNAIWAPKLQLLNGY 772	701 LSFPVAFLKFIFNEREFINRF-PTCVKHIITAGEQLVVNNEFKRYLHEHNVHLHNHY 756	773 GOSESSI-CFASNMSTEPNNMGRAVGAHSWVIDPNDINRLVPIGAVGELVIESPGI 828	GPSETHVVTTYTINPEAEIPELPPIGKPI-SNFWIYILDQEQQLQPQGIVGELYISGANV	ARDYIVPPPEKSPFFTDIPSWYPANTFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVK	GRGYLNNQELTAEKFFADPFRPNERMYRTGDLARWLPDGNIEFLGRADHQYR	IRGQRVELGAIETHLRQQMPDDLTIVVEATKRSQSANSTSLIAFLIGSSYFGNRPSDAHI	IRGHRIELGEIEBAOLLNCKGVKEAVVIDKADDKGGKYLCAYVV	DUNDATRAINIALEGVLPRHSIPSFILCMLELPRIATGKLIDKRIKLMGKDILDKQIQGA	NDSELREYLGKALPDYMIPSFFVPLDQLPLTPNGKIDRKSLPNLEGI	1009 IVQQAFARIEVEADTAAKLHSIWVQSLGIDPATVNVGATFEELGGNSTTAIKMN-MAKS 106. 1001 IVQQAFARIEVEADTA	
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1020 CMUDIPALEZAPTICELSNYTICANANGAZONYOUNG 1103   009   1121   1124	2050 QVHKEFDVELPLKVLFETPTISALAQYIADGEKGMYLAIQPVTPQDYYPVSSAQKRMYIL 2109	2056 SDEKGWTSMYDGSQIDFDEMHEWLGETTRTLHDNR 2090	IEF EGROLLING FINATE LEGUNDLIQUE ELATIONILINGE FOUNDE VONVINCING	SUCTAVSEAKEDETEQIVESFVQPFDLETAPALRVGLVKLASDRHLFLMDMHHIISDGVS	2113EVNKATESIPSL 2139 2130 MOITTKEIADLYKGKELAELHIOYKDFAVWQNBWFQSAALEKQKTYWLNTFAEDIPVLNL 2289	2140AGKAK 2144 114 115 SFEGDIVTFSAGKQLAEELKRLATETGTTLYMLLLAAYNVLLHKYSGQEE 2349	2145 VQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLA 2180 :         : :       : :       : :	2181 EDVR 2201 : 1   1   1   1   1   1   1   1   1	SQATNEHFEDMEBEL SQATNEHF	2242 LVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELSAYRY	2281AAVVHVRG 2288 2588 GVQPNSMVGIMVDRSLDMIVGMLGVLKAGGAYVPIDIDYPQERISYMMEDSGAALLLTQQ 2647	2289 SLGDELVLPVEKDDMIDFQANQLN	2313LKSSDAAIM 2328 2308 UNVAMAWKDAYRLDTFPVRLLQMASFAFDVSAGDFARALLTGGQLIVCPNEVKMDPASLY 2767	2329 AVSKIPFEITAFERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGF 2384   :   ::	2385 RVEVAVFH 2405 :::::	HCCSQGRTLVNFPTDHHLRGSDLLTNRPLQR	-LONRRIAI	2453 LLPSYMIPSNIVVLDKMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCE 2512   :       :       :   3007 DLPAAMIPSYFVSLEAMPLTANGKIDKRSL3036	2513 EATEVFGMKVDITDHFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIR 2572 3037 3036	2573 QGLGLQQPVSDGQGDRSAHMAPRTETEAILCDEFAKVLGFQ-VGITDNFFDLGGHSLMA 2631 
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	CNVDIPLELLFBAPTIQEISNYINGAKKESYVAIQPVPEQEYYPVSSVOKRMFI	LDQLDVGSLWYLIPYAVRMRGPVNVDALRRALAALEQRHETLRTFEDDDGVGYQIVHEK	1074 LNEFDRSGTAYNLPGVMFLDGKLNYRQLEAAVKKLVERHEALRTSFHSINGEPVQRVHQN	LSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLSSEAGMRATLLRLGEDDHILTIVMHHIIS :::	DGWSIDVLRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQL       : : : : :	NYWKKQLKDSSPA-KIPTDFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVL 	LAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDIIGCFVNTQOMRINIDHHDTFGTLINO	VKATTTAAFENEDIPFERVVSALQPG-SRDLSSTPLAQLIFAVHSQKDLGRFKFOGLESV	P-VPSKAXTRFDMEFHLFQETDSLKGSVNFADELEKMETVENVYRVFFEILRNGLGSSRT	1533 PVSILPLIDGIVTLEKLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRL	TYTELDRQSDILAGWLRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPS	1650 ARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDST	1707 KPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETRWAHMATIAFDGAS	1767 YELYSALLFGRTLVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVPLRVPRRLSRT :	1827 LMFFFLVVTDSTAPDAL-DAQCLYQCVQCYNGYGPTENGVMSTIYPIDSTESFI	1880 NGVPIGRALNNSGAYVVDPEQQLVGIGVWGELVVTGDGLARGYSDK-ALDENRFVHITVN :	1939 DQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVV :	1999 LQQNEDQAPEILGFVVADHDHSENDK :::::::::::::::::::::::::::::::::	2025 GQSANQVE 2038	1990 ALFARDGEFGTATETVAPSSDIEMKLAELWHNVLGVNKIGVLDNFFELGGHSLRAMTMIS 2039

102 RAFAFTSDSGKTSQVILKDSFVFSWMCWSSSSSPDEVVRDEAAAAASGPRCNRFVLLED- 160 	161MQTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPES 207 : :	208 SDATDTDSQSVSVVSMSCEDNAVSATHFWQTHLNDLNASVFPHLSDHLMVPNPTTT 263 :	264 AEHRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFGAVTEQ 308   1:1    1:1    1:1    1:1    1:1    227 APSQVSFTVDSEVSGALSAWARGQGVTMNTVVQGAWALALAQATGRDDVVFGATVSGRPP 286	309 SLPFDKHYLADGTYQTVAPLRVHCQSNLRASDVMDAISSYDDR-LGHLAPFGLRDIRNTG 367	368 DNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRALLLHCQMESSGALLV 427 :	428 AYYDHNVIDSLQTTRLLQQFG-HLIKCLQSPLDLSSMAEVNLMTE 471 ::   ::   :	472 YDRAEIESWNSQPLEVQDTLIHHEMLKAVSHSPTKTAIQAWDGDWT 517   1   1   1   1   1   1   1   1   1	518 YSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPP 577	578 ARTAQVVTQTRATVALTSKLHRETVQKLVGRCVVVDDELLQSVSASDDFSSLTK 631	632 SQDLAYVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFGA 687 	688 CLLEIMTTLINGGCVCIPSDDDRMNSIPSFINRYNVNWMMATPSYMGTFSPED 740 : :	741 VPGLATLVLVGEQMSSSVNAIWAPKLQLLNGYGQSESS-SICFASNMSTEPNNMG 794	795 RA-VGAHSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFTDIPSWY 851 :	852 PANTFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDL 911	912 TIVVEATKRSQSANSTSLIAFLIGSS-YFGNRPSDAHILDHDATKAINIKLEQVLPRH 968	969 SIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVF-ADTAAK- 1026 	1027LHSIWVQSLGIDPATVNVGATFFELGGNSITAIKMVNMAR-SVGMDLKVSNI 1077   :::::   :::   ::  ::    :	1078 YQHPTLAGISAVVKGDPLSYTLIPKSTHEGPVEQSYSQGRLWFLDQLDVGSLWYLIPYAV 1137
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TKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAEYSPFQLLF	2692 TEDPEEFMASEIKPOLELOEII-ODIYPSTOMOKAFLFDHTTARPRFVPFYIDFP	Db 3125 -TDTEQYMAIQPVSGODYYPVSSAQKRMFIVNQFDGVGISYNMP 3167  QY 2747 STSEPDAAGLIKACESLVNHLDIFRTVFAEASGELYQVVLSCLDLPIQVIETEDNI 2802  Db 3168 SIMLIEGKLERTRLESAFKRLIERHESLRTSFEIINGKPYOKIHEEADF 3216	KSMRV-IMRISHALYDGLSL :     :   :   :   EDRHVLIFDMHHIISDGISS		LSDDTVVDGNDATCKALHLSKIVNIPSQVLRGSSNIITQATVFNAACAL 295	2953 VLSRESDSKDVVFGRIVSGRQGLPVEYQDIVGPCTNAVPVRAHIE-SSDYNQLHDIQDQ   1   1   1   1   1   1   1   1   1   1	YLLSLPHETIGESDLKRNCTDWPEAITNFSCCITYHNFEYHPESQFEQQRVEMG	OY 3066 VLT-KEVNIEMDEPLYDLA-IAGEVEPDGA-GLKVTVIAKTQLEGRESFELA 3490 OY 3066 VLT-KEVNIEMDEPLYDLA-IAGEVEPDGA-GLKVTVIAKTQLEGRKRVEHLLE 3116 OH 3401 ET ACKPENIYET EURYPENI ET 1	C AND THE TAXABLE CONTROL OF THE TAXABLE CONT	130249 CDA peptide synthetase II SCE63.02c [imported] - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Nov-2000	3.; Rajandream, M	A;Accession: 130249 A;Stetus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-3670 < SAND > A;Residues: 1-3670 < SAND > A;Cross-references: PMRLAID35640. PIDN.CAR38517 1. GSDDR.GNOOTO. GCORDR.GCR63 020	Experimental source: strain A3(2) Genetics: Genetics: SCOEDB:SCE63.02c	Superramily: alpha aminoadipyl.cysteinyl.valine synthetase; acetate.coa ligase homol Keywords: carrier protein; phosphopantetheine; phosphoprotein 512-932/Domain: acetate.coa ligase homology cacli.> 948-1016/Domain: acyl carrier protein homology cacli>	7000	11.8%; Score 1906.5; DB 2; Length 3670; 23.7%; Pred. NO. 2.7-e-1102; A72; Mismatches 1086; Todals 1009. Gans 107.	45 RIEAIKPCTPFQLDMIDCNALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPAL	11

SCSTGKPGCMMTHOGICURLIAMOGITQINSIDSILORTPESPDUSUMBEFWILLTGAR 673  VCIPSDDDRMNSIPSFINRYNVMMMATPSYMGTFSPBDVPGGLAILVIVGEGDAR 75:    IVIAKPGGHDSAYLINLIIGEQITILHFVPSMLRIFLESGNVEKCTSLKRVICSGEALS 733  SSYNALWARKLGLUNGTGGSES. SIGFSARMSTERNMGRAN-ACHHGWUDD 805:   III	1458 QCKWENNCDLFTETTIHRFTEHLONILLGHTSEPSQKISDLPASGGELQJINFG 1513 1548 KLDVLNVKHVDYPRESSLADVPQTVSAYDENLAVUDSSCRLTYTELDRQSDLLAGWIRR 1607 1541 TSPTNLIHCIQELFEQQVARFGDEIAVICQHQKLTYSELNTKANQLAYHLKS 1566 1608 RSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLDVRSPSARVQDILÄGLSGLSGFTIVLI 1667 1567 LGVQPEIAVGTCVHRSLDFIIGILAILKAGGFYVPLDPTYPQERLEFLIED-AQIQVILT 1625 1668 GHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAVVLYTGG 1721 1626 QQQHIPQLPDLPIFCFDTDTAN
	40 40 40 40
peptide synthetase [Imported] - Nostoc sp. (strain PCC 7120)  0.5pecies: Moscoc sp.  1. Andre: Nacoc sp.  1. Andre: Nacoc sp.  2. Andre: Nacoc sp.  3. Andre: Nacoc sp.  4. Andre: Nacoc sp.  5. Andre: Nacoc sp.  6. Andre	1 ::

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TPSKLDEVOVRRH 1880	293	19		FREFLUQIKEKTIA 1984 VNNGINGFI 396	SDVKLSPII	OTTRLLQQFGHLIK 452	QKIAEDYFRILE 2086	LKAVSHSPIKTAIQ 510 :           EEQAKRIPDHTAVY 2145	570	::     :   : AILGVLKAGGAYLP 2204			NSDTRALQFGTHAF 685 : : : :   SONDNSSTVASTEF 2218			NMSTEPNNMGRAVG 798	DKSHQNIPIGKPID 2431	TDIPSWYPANTFPD 858	. 4		VLPRHSIPSFYICM 977	SLPDÝMIPQYFVQL 2585	FAAKLHSIWVQSLG 1036        ::   4EEKLVSIWEEALG 2634	 	FIKGLRDISVRRRK 2692	4RGPVNVDALRRAL 1152 :   ::   JEGDFDIRRFENTL 2748	121	SEKIKSFIRPFHLE 2805	NLKDSKDPLSALTP 1272 :    :    KSLKP 2856
LPEVNVOYKDYVEWNHTFNOSAAMKKOBAYWLDVYRDIPSKIDF	TAEHRITFP		YTHSDEALFGAVTEQSLPFDKHYLADGTYQTVAPLRVHCQSNLRASDVMDAIS	**************************************		QQITESSHFWPCNNRALLLHCQMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIK	IEYSTSLFKDETI	CLQSPLDLSSMAEVNLMTEYD-RAEIESWN-SQPLEVQDTLIHHEMLKAVSHSPTKTAIQ :     : : : : : : :	AWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTL		IDPNDPPARTAQVVTQTRATVALTSKLHRETVOKLVGRCVVVDDELLQSVSASDD	FFERMKIMAFDSEVRVIISDVFLABELTAESIELIH	FSSLTKSQDLAYVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAF i :	GACLLEIMTTLINGGCVCTPSDDDRMNSTPSFTNRVNVNWMMATDSVMGT		VPGLATLVLVGEQMSSSVNAIWAPKLQLLNGYGQSESSSICFASNMSTEPNNMGRAVG	NHSLRTLLTGGDKLNVFKEKSYQIVNNYGPTENTVVATSFPIDKSHQNIPIGKPID	AHSWVIDPNDINKLYPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPD	GAKLYRTGDLARYASDGSIVCLGRIDSOVKIRGORVELGAIETH-LROOMPDDLTIVVEA	::	TKRSQSANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHSIPSFYICM	REDGDHDPYLCAYVTVKKEVEPEKIRAFLKKSLPDYMIPQYFVQL	LELPRTATGKIDRRRLRIMGKDI-LDKQTQGAIVQQAPAPIPVFADTAAKLHSIWVQSLG	IDPATVNVGATFFELGGNSITAIKMVN-MARSVGMDLKVSNIYQHPTLAGISAV-VKGDP 	INKIGINSHFFEAGGHSLKAAALVSTIHKELNVKLPLRQIFETPTIKGLRDISVRRK	LSYTLIPKSTHEGPVEQ-SYSQGRLWFLDQLDVGS-LWYLIPYAVRMRGPVNVDALRRAL	AALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLS	RHESFRTSFVMIDGEVMQQIEKEIDFQVAYSDIGKESAE	SEAGWRATLLRIGEDDHILTIVMHHIISDGWSIDVLRRDLNQLYSAALKDSKDPLSALTP    :::    ::    :              ::        KAPLLRAEVVKLNEREHLLMFDMHHIISDGVSTDIFIQELGALYEGKSIKP
1830 LPEV	251	1881 HIDT	294 YTHS			397 QQIT	2038 FELD	453 CLQSI : 2087 EVSEI	511 AWDGI	2146 FEDQI	571 IDPNI		626 FSSL7 :: 2259 IDNV			741 VPGLA	2376 NHSLI	799 AHSWI 2432 NVKV)	859 GAKLN	::  2483 GERMY	918 TKRSC	2541 REE	978 LELPR 	7	2635 INK	1095 LSYTI   2693 CFY			1213 SEAGW 2806 KAPLI
qq	Qy	qq	oy d	} Å	qq	Oy	qq	QY Dp	οy	qq	Qy	3 ,	O Dp	, AO	qa	οy	qq	Qy Db	, VO	qa	Οy	qa	Oy Dp	· Oy	qq	oy Oy	δο i	g ,	Qy D <b>b</b>

1273 LPIQYSDFAKWQKDQFIEQE--KQLNYWKKQLKDSSPA-KIPTDFARPALLSGDAGCVHV 1329 1330 TIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLFAVEDAVIGTPIANRNRPELEDII 1389 GCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQPGSRDLSSTPL 1449 METVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVL-NVKHVD--YPRESSL 1565 1566 ADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWLRRRSMPAETLVAVFAPRSCE 1625 1450 AQLIFAVHSQKDLGRFKFQGLESVPVPSK-AYTRFDMEFHLFQETDSLKGSVNFADELFK 1508 : |: |: |: || | | 3034 | 3036 FDTMLVYHN-TDVKPFEAEGLRSRLVEIKRGISKFDITVTASEAADGLRLEVEYSTTLFN 3094 ::|:| || || || || || 3152 PELFEKQAEKTPDHPAVARGDETISYRELNERANSLAFTLRQKGVGPDVIAGILTERSIE 3211 1626 TIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVR 1685 1686 IRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVI---IRTVTS 1742 1743 GCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALKDVFFREHV 1802 3383 N-----VSDMTPAHLNMLAYVDKTELEFDVKELIVGGDALTPDVIG--GLFHKFPNLSCN 3435 1855 -YNGYGPTENGVMSTIYPIDS----TESFINGVPIGRALNNSGAYVVDPEQQLVGIGVM 1908 3436 ITNVYGPTECCVDAASHQIESGKVPQTPS----IPIGRPLLNTSIYIVDKELRPLPVGIA 3491 1909 GELVVTGDGLARGYSDK-ALDENRFVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMD 1967 1968 TQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVVADHDHSENDKGQS 2027 2088 DNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEPSRSAAAFVNKATESIPSLAGKAKVQV 2147 2198 GDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELL-VEPAFFTSLKDRFP 2256 1803 NAASHVTSSSQDVPLRVPRRLSRTLMFF----FLVVTDSTAPDALDAQGLYQ---GVQC- 1854 2028 ANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLH 2087 3765 HFNQSFWLFRKDGYDENIVRTAFNKILEQH------DALRMIYEEKDGDIIQYNRGYREN 3818 2148 GTATDIGQVDDLHPDLVVLNSVIQYFP-----SSEYLAEIADTLIHLPNVQRIFF 2197 3705 AKMNLKLEMKALFANPKIKDLSRFITEETRHRKHNKPVTGETELLPIQKRYFANNKEELD 3764 GLVEHVEILPKNMEAVNEL-SAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKS 2315 3610 LER-----VKLDRLPR-------1390 1509

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site: phosphopantetheine (Ser) (covalent) #sta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: | : : | : OGTERTNYPLCLSVNDYGSELDLIIHSMQPANPQR 3601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRVHCQSNL----RASDVMDAISSYDDRLGHLAPF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OGSHVNN----GINGFLOOITESSHFM-PCNNRA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMT 470
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                                                                                             3510628; PID:93510629; PIDN:AAC80285.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDTRALQFGTHAFGACLLEIMTTLINGGCVC---- 703
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                                                                                                                                               ggy; acyl carrier protein homology cetheine; phosphoprotein nology <ACL1>
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No. 8.8e-100;
smatches 1202; Indels 1171;
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homology «ACP3»
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Nature 406, 959-964, 2000  A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A; Reference number: A82950; MUID:20437337; PMID:10984043  A; Reference number: R8345  A; Status: preliminary A; Molecule Uppe: DNA A; Residues: 1-5149 <sto> A; Cross-references: GB:AE004667; GB:AE004091; NID:g9948444; PIDN:AAG05790.1; GSPDB:G1 A; Experimental source: strain PAO1 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; GB:AE004091; NID:g9948444; PIDN:AAG05790.1; GSPDB:G1 C; Superfamily: acyl carrier protein homology; acetate-CoA ligase homology C; Keywords: carrier protein; phosphopantetheine; phosphoprotein F; 579-998.Domain: acetate-CoA ligase homology <acd1> F; 2034-2479/Domain: acetate-CoA ligase homology <acd2> E; 2034-2479/Domain: acyl carrier protein homology <acd2> E; 2034-2479/Domain: acyl carrier protein homology <acd2> E; 2046-2564/Domain: acyl carrier protein homology <acd2> E; 2064-2556/Domain: acyl carrier protein homology <acd2> E; 2064-2566/Domain: acyl carrier protein homology <acd2> E; 2064-2667/Domain: acyl carrier protein homology <acd2> E; 2064-267/Domain: acyl carrier protein homology <acd2> E; 2064-267/Domain</acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd2></acd1></sto>	F:3084-302A/Domain: acyl carrier protein homology <acl>&gt; F:3084-302A/Domain: acyl carrier protein homology <accp>&gt; F:3583-5040/Domain: acetate-CoA ligase homology <accp>&gt; F:4583-5040/Domain: acyl carrier protein homology <accp>&gt; F:5057-5125/Domain: acyl carrier protein homology <accp><acpp>&gt; F:1047,2528,3573,5089/Binding site: phosphopantetheine (Ser) (covalent) #status predictionery Match    11.6%; Score 1867.5; DB 2; Length 5149;</acpp></accp></accp></accp></accp></acl>	Best Local Similarity 25.2%; Pred. No. 9.8e-100; Matches 835; Conservative 518; Mismatches 1339; Indels 625; Gaps 134;  Qy 16 TPASFCSHGDSPL-NSSYEQLFHLYGLDSSRIEAIKPCTPFQLDMIDCNALDKQSAIGHA 74	. Qy 75 VYDVPTDIDISREALAWKEIVNQTPALRAFAFTSDSGKTSQVILKDSFV 123 ::               :	QY 124 FSWMCWSSSSPDEVVRDEAAAASGPRCNRFVLLEDMQTKKCQLVWTFSHALVDVTF 181	QY 182 QQRVLSRVFAAYKHEKDTHRPETPESSDATDTDSQSVSVVSMSCEDNAVSATH 234 :: :     ::     ::   1   1   1   Db 1686 NAQLLAEVLQRYAGQEVAATVGRYRDYIGMLQSRDAKATES	QY 235 FWQTHLNDLNASVFPHLSDHLMVDNPTTTAEHRITFPLSGKALSNSAICRT 285	Qy 286 ALSILLSRYTHSDEALFGAVTEQSLPFDKHYLADGTYQTVAPLRVHCQSNLRASDVM 342   ::   ::     :   :   :   :   :   :	Qy 343 DAISSYDDRLGHLAPFGLRDI-RNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQ 398  1843 QGMQALNLALREHEHTPLYDIQRWAGHGGEALFDSILVFENFPVAEALRQAPADLEF 1899	Qy 399 ITESSHEMPCNNRALLLHCQMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQS 456	Qy 457 PLDLSSMAEVNLMTEYDRAE-IESWNSQPLEVQDTLIHHEMLKAVSHSPTKTAI 509 : ::  :  :	Qy 510 QAWDGDWIYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFT 569    1
6083 ATSYELFDVLPDTLSLPIGKPNANVRVYLDARREPVPMGVVGDIYIGGTGVALGYLNRP 6142 2363SAE	,		2732 TARPRPFVPFYIDFPSTSEPDAAGLIKACESLVNHLDIFRTVFAEASGELYQVVLSCLDL 2791   1   1   1   1   1   1   6419	OY 2792 PIQVIETEDNINTATNEFLDEFAKEFVKLGH-PLIRFTIKQTK 2834  :	2835 SMRVIMRIS-HALYDGLSLEHVVRKLHMLYNGRSLLPPHQFSRYMQYTADGRESGH 2889 :::	2890 GPWRDVIQNTPMTILSDDTVVDGNDATCKALHLSKIVNIPSQVLR 2934	2935 GSSNIITQATVFNAACALVLSRESDSKDVVFGRIVSGROGL 2975   1   1   1   1   1   1   1   1   1	2976 PVEYODIVGPCTNAVPVRAHI-ESSDYNQLLHDIQDQYLLSLPHETIGFSDLKRNCTDWP 3034   ::::    :    :	3035 EAITHFSCCITYHNFEYHPESQFEQQRVEMGVLTKFVNIEMDEPLYDLAIAGE 3087 :::	QY 3088 VEPDGAGLKVTVIAKTQLFGRKRVEHLLEEVSKTFEGL 3125 :   :             Db 6773 LASENGALNGVIEYASDLFDRSTVERFKQHFHTLLEAWVEDVAQPVLGL 6821	FESULT 12 FR3345 FR3345 FR3345 C;Species: Pseudomonas aeruginosa C;Species

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2123 PLPEVAGETLAYVIYTSGSTGQPKGVAVSQAALVAHCQAAARTYGVGPGDCQLQFASISF 2182	686 GACLLEIMTTLINGGCVCIPSDDDRNNSIPSFINRYNVNWMMATPSYMGTFSPE 739	2183 DAAAEQLFVPLLAGARVLL-GDAGQWSAQHLADEVERHAVTILDLPPAYLQQQAEELRHA 2241	740 -DVPGLATLVLVGEQMSSSVNAIWAPKLQL-LNGYGQSESSSICFASNMSTEPNNMG 794 : :     :     :     :  :     :  :     :  :	795 RAVGAHSWVIDPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPAN 854	2302 RALGARRACILDAALQPCAP-GMIGELYIGGQCLARGYLGRFGQTAERFVADPFS 2355	855 TFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIV 914   :	SSSYFGNRPSDAHILDHDATKAINIKLEQVLPRHS	2409 AEAAVVALDGVGGPLLAAYLVGRDA-MRGEDLLAELRTWLAGRLPAYMQPTA 2459	YICMLELPRTATGKIDRRRLRIMGKDI		1034 SLGIDPATVNVGATFFELGGNSITA.KMVNMAR-SVGMDLKVSNIYQHPTLAGISAVVKG 1092	YTLIPKSTHEGPVEQSYSOGRLWFLDQLDVGSLWYLIPYAVRMRGPVNVDAL	::      :	1149 RRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCG-SDLDPFEVLNOEQTT 1207	2624 QQAFDWLVLRHETLRTRFEEVDGQARQTILANMPLRIVLEDCAGASEATLRQRVAEEIRQ 2683	1208 PFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDLNQLYSAALKDSKDPL 1267	2684 PFDLARGPLLRVRLLALAGQEHVLVITQHHIVSDGWSMQVMVDELLQAYAAARRGEQ:2740	1268 SALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSPA-KIPTDFARPALLSGDA 1324		: : :   :	1385 LEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFENEDIPPERVVSALQPGSRDL 1444	FILILI : : : : : : : : : : : : : : : : :	1445 SSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTREDMEFHLFQETDSLKGSV 1500     - - - - - - - - - - - - - - - - - -	NEADET DEED INC. TO CONTRACT OF THE PROPERTY O	1901 REALDLERAIN ENNYNYNYE FILKNOLOSSKIPVOLLELIOLOVILERLINDLNYKHUNYP 1960 1901 - 1 11: 1 1 1: 1 1 1: 1 1 1: 1 1 1 1 1			FFGVLKANL	3096 ERSIEMVVALMAILKAGGAYVPVDPEYPEERQAYMLEDSGVQLLLSQSHLKLPLAQGVQR 3155	1681 VEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTV 1740 ::::
qα	Oy	qa	. Qy	QY	q	Oy Op	ογ	QΩ	δō.	Q C	Oy Op	οy	ΟÞ	Οy	QQ	Οy	ପ୍ର	Oy Dp	Qy	ΟD	Oy	QQ	oy du	è	5 A	δλ	qq	Qy	QQ	Oy Dp

δy	1741	TSGCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYM 1785
qq	3206	SNRLCWMQQAYGLGVGDTVLQKTPFSFDVSVWEFFWPLMSGARLVVAAPG 3255
۵y	1786	TTLDARALKDVFFREHVNAASHVTSSQQDVPLRVPRRLSRTLMFFFLVVTDST
QQ	3256	DHRDPAKLVALINREGVDTLHFVPSMLQAFLQDEDVVSCTSLKRIVCSGEALS 3308
λά	1840	PDALDAQGLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSG 1892
qo	3309	ADAQQQVFAKLPQAGLYNLYGPTEAAIDVTHWSCVEEGKDAVPIGRPIANLG 3360
Σγ	1893	TVKAY
و	3361	CYILDGDLEFVPVGVLGELYLAGRGLARGYHQRPGLTAERFVASPFVAGERMYRTGD 3417
λζ	1950	RVRYRIGDGLIEFFGRMDTQFKIRGNRIESABIEAALLRDSSVRDAAVVLQQNEDQAPEI 2009
qc	3418	LARYR-ADGVIEYAGRIDHQVKLRGLRIELGEIBARLLEHPWVREAAVLAVDSRQL 3472
λχ	2010	LGFVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGW 2061
qc	3473	
۶y	2062	TSMYDGSQIDFDEMHEWLGETTRTLHDNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEP 2121
qc	3533	GQTHVAPQNEMERRIAAVMADVLKLEEVGATDNFFALG-GDSIVSIQVVSRCRA-AGIQ- 3589
27	2122	SRSAAAFVNKATESIPSLAGKAKV-QVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLA 2180
qc	3590	G 3619
λy	2181	EIADTLIHLPNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEE 2240
qc	3620	PASGETVLLP-FQRLFF
λγ	2241	FPG
q	3649	
λy	2298	VEKDDMIDFQANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAFERQV 2344
qc	3704	AEAVDRQALESI.CEESQRSLDLADGPILRSLLVDMADGGQRLL 3746
λλ	2345	VASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSARGWSQ 2396
q	3747	VIHHLVVDGVSWRILLEDLQRAYQQSLRGEAPR
	2397	NGALDAVFHHCCSQGRTLVNFPTDHHLRGSDLLTNRPLQRLQN 2439
q	3793	GRVSEHARGESMKAQLQFWRELLEGAPAELPCEHPGGALE 3832
λ	2440	ERL-RSLLPSYMIPSNI
q	3833	RFATSVQSRFD
λλ	2499	
ą	3883	:     :
	2555	VKDVFDHPVFADLASVIRQGLGLQQPVSD-GQGQDRSAHMAPRTETEAILCDEFAKVLGF 2613
q	3919	PV-ADLGESLKAIKEQLRAIPDKGLGYGLLRYLAGEESARVLAG 3961
λλ	2614	FDLGGHSLMATKLAV~RIGHRLDTTVSVKDVFDHPVLFQ
ą	3962	LPQARITFNYLGQFDAQFDEMALLDPAGESAGAEMDPGAPLD 4003
γ	3666	NLVQSKTNEIVGGREMAEYSPFQLLFTEDPEEFMASEIKPQL
q	4004	NWL-SLNGRVFDGELSIDWSFSSQWFGEDQVRRLADDYVAELTALVDFCCDSPRHGATPS 4062

SGPRCNRFVLLEDMOTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTH	GHLAPFGLRDIRNTGDNGSAADFQTVILVTDGSHVNNGING RTLGSQPYEHVPLYDLQSVLKQELIDHLLVIENYPLVEALQKKALNQQIG  FLQQITESSHFMPCNNRALLLHCQMESSGALLVAYYDHNVIDSLQTTRLLQQF-GHLIKC	511 AWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTL 570  1	627 SSLTKSQDLAYVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALQFGTHAFG 686	790 PNNMGRAV-GAHSWVIDPNDINRLVPIGAVGELVIESPĞIARDYIVPPPPEKS 841	962 EQULPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQTQGAIVQQAPAPIPVFA 1023
E 2750 R 4115 A 4166 L 2850 W 4226 L 2904 L 4278 S 2955	Db 4279 DEPTRLVEGALAQPGLTSANGGGEHLREVDATATARIRDFARRHQVTLNTLVQAGWALLLQ 4338  Qy 2956 RESDSKDVVFGRIVSGROG-LP-VEYQDIVGPCTNAVPVRAHI-ESSDYNOLLHDIDODOY 3012  Db 4339 RYTGQHTVVFGATVSGRPADLPGVENQVGLFINTLPVVVTLAPQMTLDELLGGLQRQN 4396  Qy 3013 LLSLPHETIGFSDLKRNCTDWPEAITNFSCTITYNNFEYHPESQFEQQRVEMGVLTK 3069  Qy 3013 LLSLPHETIGFSDLKRNCTDWPEAITNFSCTITYNNFEYHPESQFEQQRVEMGVLTK 3069  Db 4397 LALREQEHTPLFELQRWAGFGGEAVFDNLLVFENYPVDEVLERSSAGGVR 4446  Qy 3070 FVNIEMDEPL-YDLAIA 3085	:	C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 03-Nov-2000 C;Accession: T31075 R;Mootz, H.D.; Marahial, M.A. J. Bacteriol. 179, 6843-6850, 1997 A;Title: The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequ A;Title: The tyrocidine biosynthesis operon of Bacillus brevis: Depth of A;Title: The tyrocidine biosynthesis operon of Bacillus brevis: Depth of A;Title: The tyrocidine biosynthesis operon of Bacillus brevis: Depth of A;Title: The tyrocidine biosynthesis operon of Bacillus brevis: Depth of A;Title: The tyrocidine sequence and the tyrocidine biosynthesis operon of Bacillus brevis: Omposition of A;Title: The tyrocidine sequence and the tyrocidine of the tyrocidine sequence of the tyrocidine sequence of the tyrocidine sequence of the tyrocidine of the tyrocidine sequence of th	ology;	7; 18; Gaps PYDIDISRFA  : :    GDLDVGLFT VYRDEAAAAA :

	2173 2173 2259 2208 2319 2234 2379	2261 2437 2293 2497 2320 2557	2617 AGGAFLPVDPDYPEE 2415VNFPT 2670 YATQTDNLPCANTPS 2424RG 2730 HFASISFDASVWDMF	2460 2790 2499 2846 2532 2906	QY         2560DHPVFADLASVIRQGLGL           Db         2966 EDDRGQAYLCAYVAGGEATPAQLRAYME           QY         2592HMAPRTETEAILCDEFA           SD         3026 PKPNQEENRTEQYAAPQTELEQILAGIWA           QY         2639 GHRLDTTVSVKDVFDHPVLFQLAGILAGIWA           Db         3086 -NASGWTLAMKELFQYPTIEBAALRV           QY         2699 MASEIKPQLELQEIQDIYPSTQMQKAFL           QY         2699 MASEIKPQLELQEIQDIYPSTQMQKAFL
1140 RGPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLC   1191	1203 FSELYON	1488 HLFQETDSLKGSVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVTLE 1547  :	1665 VLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGS 1722	1831 FLUVTDSTAPDALDAQGLXQG	1990 SSVRDAAVVLQONE
oy da bb	40 VO VO VO VO VO VO VO VO VO VO VO VO VO	0 O O O O O O O O O O O O O O O O O O O	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Oy Oy Oy Oy	, dd dd dd dd dd dd dd dd dd dd dd dd dd

AFER-----QVVASLNSNIDEWQLSTIRSSA 2364 | || : :: :: 3436 CHQDYPFESLVEKLGIPRDPGRNPLFDTMFILQ 2436 DLSFHLTERETDLFLRLEYCTKLFKQQTVERM 2496 FNLDSRLESYVGLEPSR---SAAAFVNKATES 2135 DIGOVDDLHPDLVVL----- 2172 HL----- 2207 RAVDVPTDFPRPAVKSFAGGQVTLSMDQELLSA 2318 ----FTSLKD-----RFPG-----LVE 2260 AAVVHVRGSLGD----- 2292 /EK-----DDWIDFQANQLNQ---KSLGDL 2319 AVLREKGVGPAQIVALLVERSAEMVIATLATLK 2616 SSARQWSQNGALDAVFHHCCSQGRTL----- 2414 SQAKLVVTHAHL---LHKVSSQSEVVDVDDPGS 2669 ----- 2423 SKPKGVMLEHKGVANLQAVFAHHLGVTPQDRAG 2729 2N-----PRIAIEVRERLRSLL---PSYMI-- 2459 SRDVINDFQRFAEYVRDNAITFLTLPPTYAIYL 2789 ----LNANGKVDRKELSRRAKVVPKQQTAAPL 2498 SKVTYVNGYGPTESTVCATLWKAKPDE----PV 2845 : ::| : :205 )RLKVR---- 2559 ::|:| HQVKIRGHRVELGEVESVLLRYDTVKEAAAITH 2965 ------20PVSDGQGQDRSA- 2591 ALVQSKTNEIVGGREMAEYSPFQLLFTEDPEEF 2698 ----- IPNSRE---- 3116 FLEDHTTAR---PRPFVPFYID-FPSTSEPDAA 2754 

	522 DNVSSRLAVHIKSLGLRAQOALIPUYFEKSKWYIASMLAVLKSGNAFTLIDPUPPARTA 581  4309 DGGANQTARHILGEGIGAED-FVAIALAKSLDAVISMLAVLKTGAATLIDPUPPARTH 4367  582 QVYQTRATYALTSKLHRETYQKIUGRCVVVDDELLQSVSASDDFSSLTKSDLAVYI 639  ::
Db 3117SE	REBULT 14 Ty5614 COA Peptide synthetase I - Streptomyces coelicolor C. Species: Streptomyces coelicolor C. Species: Streptomyces coelicolor C. Species: Streptomyces coelicolor C. Species: Streptomyces coelicolor C. Dete: 03-Dec-1999 #text_change 01-Dec-2000 C. Accession: T36248 A. Reterence number: 221602 A. Accession: T36248 A. Rotecher on muber: 221602 A. Accession: T36248 A. Rotecher on T36248 A. Rotecher on T36248 A. Rotecher on T36248 A. Rotecher on T36248 A. Rotecher on T36248 A. Rotecher on T36248 A. Accession: T36248 A. Rotecher on

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RESULT 15 C69681 peptide synthetase ppsC - Bacillus subtilis	2129 VNRATESIPSLAGRAKVQVGTATDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIADTLIH 2188 F 1 :	da da
	V 5738	q <sub>0</sub>
3107 GRKRVEHLLEEVSKTFEGL 3125   1	QIDFDEMHEWLGETTRTLHDNRSLGNVLEIGTGSGMILFNLDSRLESYVGLEPSRSAAAF         :1:	6y
6241 STAETDPDASLALPGLRVGAERS		r q
	ILGEVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGS	oy S
6185	1949 DRVRYRIGDGLIEFFGRMDTGFKIRGNRIESABIEAALLRDSSVRDAAVVLQQNEDQAPE 2008    1   1   1   1   1   1   1   1   1	oy D
2994	YVLDSALRPVAPGVTGELYLAGEQLARGYLGRPALTAERFTANPHSSTPGARMYRTG 5673	g ,
6128	VTGDGLARCYSDK-ALDENRFVHITVNDQTVKAYRTG 1948	δδ :
2934	5558 GEALHTDHLATWRTQHPCAQIINAYGPTESTVNITDHHV-SEDTPDGPVPIGRPFANTQV 5616	Dp
Z884GRESGHGEWRDVIQNTPMTI-LSDD-	1840 PDALDAQGLYQCVQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGA 1893	οy
. 6010 VLLL	5517 HLTSLEBABVQPSLIKATPSHLPLLTTLPETASPSHTLILG 5557	dÖ.
2838	DVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTA 1839	δy
5957 IHAWEPGMLPLGVVDTGEGELDAMLSAGVHHA		o Q
2786 LSCLDLPIQ	RDKCVMTEHBUTT TOTAL TOTAL THE THE THE THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE	ò
:   :   :	1000 LIGHDTAFPDLEVINVEFVKIKDALNISNADGFEVIEHDSTKP-SATSLAYVLTSGSTG 1724  1   1   1   1   1   1   1   1   1   1	g g
2728 FDHTTAR	LGEGLGAEDFVAIALAKSLDAVISMLAVLKTGAAYLPIDPDYPAERITYML 5410	අ ද
	1606 RRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIV 1665  -         :   :   :	ΟŅ
5814	5301 ERVLVEWNGAPTQLP-GTPLHELISEQARLTPDAVAVVCDGTTLTYAELDRRANQLARHL 5359	QQ
	1605	δý
Db 5795	SFDTSRRPQGIEAALDFSTELLDRRSAQAIADRFLRVLEAVTTAPDRPIGAVELMDPAER 5300	og o
2549 LKVRITVKDVFDHPVFADLASVIRQGLGLQQF	3162 LNF-AKTLENHFLEQVLLIFNNTDHEGALKULSELFGLIVALKEVQRISSKFDLSFGFAE 5240  1492 ETDSLKGSVNFADELFKMETVENVRVFFFTI.RNGTOGSPADVSTI.BT-MAGTVF 1545	3 8
5784	LOPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLE-SVPVPSKAYTREDMEFHLFQ 1491	y a
DD 5/50	5122	QQ
2429 LTNRPLORLONRRI	QCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSA 1436	QY
		d d
7 2369 SLSVPDIFRIAGEAGFRVEVSSARQWSQNGAL		ò
Db 5745	1265 DPLSALTPLETQYSDFAKWOKOQFIEGEKOLNYWKKOLKD-SSPAKIPTDFAR 1316   1	y d
	5003	qq
Y 2249 ISENDRE FOLVENVELLERNNMERVNELSALRI	1264	οy
0/40	FTEDERGAYQIVLPVEAASTPFTVVDVAEEEIGDRLDEA 4944	qa
OY ZIBS LPNVORIFFGDVRSQATNEHFLAARAIHTLG	1204	Qy
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Qy.	2189	LPNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFF 2248
qq	5745	5744
οy	2249	TSLKDRFPGLVEHVEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQA 2308
qq	5745	5744
Qy	2309	FERQVVASLNSNIDEW
QQ	5745	11 7747
Qy	2369	DHHLRG
qq	5748	9149Pd
οy	2429	LTNRPLORLONRRIAIEVRERLRSLLPSYMIPSNIVVLDKMPLNANGKVDRKELSRRAKV 2488
Dρ	5750	
οy	2489	EVEVILCEEATEVFGMKVDITDHFFNLGGHS
Db	5784	TALPAPAYSAS 5794
Οy	2549	63
Db	5795	TPRTPREEI
Qy	2609	TDNFFDLGGHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLA
Db	5814	EVLGVDLVTIDDNFFDLGGHSLLATRLVSRARTALGVELSVRQFFETPTIAGLSGAFDR- 5872
Qy	2668	SYSPFQLLFTEDPEI
qq	5873	
Οy	2728	TTARPRPF VPFY IDFPSTS
QQ	2900	FLHQLEGPSATYNIPTTLRLTGTLDTDALQSALNDLLARHESLRTTYTE-DGEGPRQV 5956
Οy	2786	LPIQVIETEDNINTATNEFLDEFAKEPVRLGHPLIRFTIIKQT
Db	5957	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy	2838	KEHMEYNGRSEEP
qq	.6010	:
Oy	2884	GRESGHGFWRDVIQNTPWTI-LSDDTVVDGNDATCKALHLSKIVNIPSQVL 2933
QQ	0209	DADAPAGRQLAYWTRQLADLPEQLDLPTDRPRPAVASQDGDRVAFSLDADLYVRLTEL 6127
ογ	2934	NIITQATVFNAACALVLSRESDSKDVVFGRIVSGRQGLPVEYQ
qq	6128	ARATHSST-FMVVQAALAVLLTRLGAGEDIPIGTPVAGRTDDATENLVGFFVNTLVLR 6184
Qy	2994	IGESDLF
qq	6185	: :   : :   PTFRELLEETRRTDLAAYAH
Οy	3047	HNFEYHPESQFEQQRVEMGVLTKFVNIEMDEPLYDLAIAGEVEPDGAGLKVTVIAKTQLF 3106
QQ	6241	DPDASLALPGLRVGAERSRLGAAKVD
Qy	3107	GRKRVEHLLEEVSKIFEGL 3125
qq	6301	DRSTARSLVERFVRTLEAV 6319
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  ----GLRDIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITE 401
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                                                                                                                    YS----CSVKVIPGRTLYVRIHFQTSA-----YQPSMMSEIKDYLL-----HMVSDVIS
                                                                                                                                                                           PLDLSSMAEVNLMTEYDRAEIESWNSQPLEV--QDTLIHHEMLKAVSHSPTKTAIQAWDG
                                                                                                                                                                                                     DPSL-PVSKMTLLDEDKTRKIVSQNNRTVSVSPEAPTLHGLFERQAAVTPERLAIRFSGG
                                                                                                                                                                                                                                                                DWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPN
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Y, M.; Nogawa, K.; Ogihara, A.; Odaga, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
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Microbiology 141, 645-648, 1995
A; Title: A putative new peptide synthase operon in Bacillus subtilis: partial characteri A; Reference number: 140454; MUID:95227362; PMID:7711903
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F;510-953/Domain: acetate-CoA ligase homology <ACLI>
F;970-1038/Domain: acyl carrier protein homology <ACE>
F;151-1990/Domain: acetate-CoA ligase homology <ACLE>
F;2006-2073/Domain: acyl carrier protein homology <ACPE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;2006-2073/Domain: acyl carrier protein homology <ACF2.
F;1002,2038/Binding site: phosphopantetheine (Ser) (covalent)
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Superfamily: peptide synthetase ppsD; acetate-CoA ligase
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peptide synthetase 3
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Residues: 1-859 <RES>
  N; Alternate names:
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3 6		ODI 130	
oy Dp	1429 PFERVVSAI     :     370 PFEELVDKI	PFERVSALOPGSRELSSTEILSTHAOLIFAVHSQKDLGRRKFQGLESVPVPSKAYTREDME 1486	
Oy Db	1487 FHLFQETDS	FHLEOETDS-LKGSVNFADELFKMETVENVRVFFEILRNGLOSSRTPVSILPLTDGIVT 1545 : :: :: :: :: :: :: :: :: :: :: :: :: :	
QY		160	
qq	:    1488 HYLIHELNF		
Oy	1606 RRRSMPAET	RRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIV 1665	
Dp	1548 QIKGVGPDS	WVALLTGRTPELJAGMLGILKAGGAYLPIDSNLPVERIAYMLSDSRAAL 1605	
Qy Db	1666 LIGHDTAPE  : : 1606 LLQSEKTER	LIGHDTAPPDIEVINVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGR 1725 	
٥y	1726 PKGVMIEHF	178	
QQ	1660 PKGVMIEQE	:       :      :   :	
Qy	1786 TTLDARALK	TTLDARALKDVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALD- 1844	
pp	1720. TFLDSHQLK	TPLDSHOLKRYIEHQGITTIWLTSSLFNHLTEQNEQIFSQLKHLIIGGEALSPSHVNR 1777	
Qy	1845 AQGLYQGVQ	AQGLYQGVQCYNGYGPTENGVWSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVG 1904	
Db	1778 IRNVCPEVS	: :	
λo		IGVMGELVVTGDGLARGYSDKA-LDENRFVHITVNDQTVKAYRTGDRVRYRIGDGLIE 1961 	
qq	1836 VGAVGELCV	GGDGVARGYLGRPDLTKEKFVPHPFAPGDRLYRTGDLARW-LSDGTIE 1891	
Qy	1962 FFGRMDTQF	FFGRMDTQEKIRGNRIESAEIEAALLEDSSVRDAAVVLQQNEDQAPEILGFVVADHDHSE 2021	
Д	1892 YVGRIDDQV	KVRGYRVELGEIETALRQIDGVKEAAVLARTAQTGSKELFGYISV 1945	
Oy	2022 NDKGQSANQVE-	VEGWODHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGS 2068	
qq	1946 -KAGTNAEQ		
QY	2069 QIDFDEM	HEWLGETTRTLHDNRSLG	
DP	2005 RNELEEQLA	RNELEEQLALIWQEVLGIQRIGIEDSFFELG-GDSIKALQVSARLGRYGLSLQVS 2058	
QY	2123R	RSABAFVUKATESIPSLAGKAKVQVGTATDIGOVDDLHPDLVVLNS 2168	
QQ	2059 DLFRHPKIK	DLFRHPKIKDLSPFIRKSERITEQGPIQGDV-PWTPVQQWFFSQDIEERHHFNQ 2111	
QY	2169 VIQYF	SSEYLAEIADTLIHLPNVQRIFFGDVRSQATNEHFLAA 2212	
Db	2112 SVMLFHSGR	SVMLFHSGRLSENALRPALKKLAEHHDALRWYRNDDRRWIQINQGIHESQLYS 2165	
Qy	2213 RAIHTLGKNAT	KDDVRQKMAELE	
QQ	2166 LRISDLSQS	LRISDLSQSESGWETKIRQEVADLQQSINLQEGPLLHAALFKTLTGDYLFLAIHHLVVDG 2225	
Oy	2262VEILPKN	VEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDL 2319	
Db	2226 VSWRILLEDLSA	LSAGYQQAAAGQTIQLPPKTDSYQEY-ARRIQEYAQSSK 2272	
Οy	0	AVSKIPFEITAFERQVVASLNSNIDEWQLSTIR-SSAEGDSSLSVP 2373	
Dβ	273	LIREEAYWRSVEEQQAAELPYEIPHHVNIDFSKRDSLSFSLTEADTAVLLQ 2323	
Qy	2374 DIFRIAGEA	DIFRIAGEAGERVEVSSARQWSQNGALDAVFHHCCSQGR 2412 ::   :::  ;::	

Search completed: May 30, 2003, 12:50:02 Job time : 164 secs

May 30, 2003, 12:39:11 ; Search time 161 Seconds (without alignments) 4004.481 Million cell updates/sec US-09-482-788-2 16128 1 MEYLTAVDGRQDLPPTPASF.....RVEHLLEEVSKTFEGLNSSL 3129 671580 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 671580 seqs, 206047115 residues Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\* 1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\* sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\* sp\_archeap:\* sp\_plant:\* sp\_rodent:\* sp\_mammal:\* sp\_virus:\* SPTREMBL\_21:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q00869 fusarium eq	009164 tolypocladi	Q00868 gibberella	P97961 cylindrotri	Q918h4 streptomyce			Q9k5m1 anabaena sp	Q01135 metarhizium	Q9uvn5 alternaria	005647 streptomyce	Q9rah2 nostoc sp.	Q9rah4 nostoc sp.	Q44928 bacillus br	Q9z4x5 streptomyce	Q8ytr5 anabāena sp
ID	698000	009164	000868	P97961	Ф9г8н4	007944	Q9FB33	Q9K5M1 ·	001135	Q9UVN5	005647	Q9RAH2	Q9RAH4	044928	Q924X5	Q8YTR5
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% Query Match Length DB	3131	15281	983	1051	4247	4848	2841	5060	5157	4360	1997	3317	4379	4450	3670	2588
& Query Match	61.2	31.0	17.8	15.5	14.8	14.1	13.3	13.1	12.5	12.4	12.3	12.3	12.2	12.0	11.8	11.8
Score	9874	2000	2871	2496	2391	2275.5	2146.5	2108	2018.5	2002	1984	1978.5	1974	1933	1906.5	1896.5
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                              YGQSESSSICFASNM---STEPNNMGRAVGAHSWVIDPNDINRLVPIGAVGELVIESPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLYRTGDLARYASDGSIVCLGRIDSQVK
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                                                               Gaps
                                                              86;
                                               Length 3131;
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                                  346494 MW; AD7663E91FAB67C4 CRC64;
                                                                                                              Ξ
                                                              Mismatches 680;
                                                DB 3;
Pfam; PF00550; pp-binding; 3.
PROSITE; PS50075; ARP_BODMAIN; 6.
PROSITE; PS00455; AMP_BINDING; 2.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_3
                                                Score 9874;
Pred. No. 0;
                                                              448;
                                               61.2%;
                                                              Conservative
                                  3131 AA;
                           Phosphopantetheine.
                                                       Similarity
                                                       Local Simines 1959;
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1068 1127 1180 1247 1240 1305 1365 1359 1425 1419 1485 1479 1545 1539 1845 1187 1605 1665 1725 1785 1833 1905 1892 1965 1952 2012 1774 2023 ----EKNSHI LDHDATKAINIKLEQVLPRHSIPSFYICMLELPRTATGKIDRRRLRIMGKDILDKQTQGA IVQQAPAPIPVFADTAAKLHSIWVQSLGIDPATVNVGATFFELGGNSITAIKMVNMARSV GMDLKVSNIYQHPTLAGISAVVKGDPLSYTLIPKSTHEGPV-EQSYSQGRLWFLDQLDVG SLWYLIPYAVRMRGPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKV IDLCGSDLDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDV LRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKD--QFIEQEKQLNYWKKQLKDS SPAKIPTDFARPALLSGDAGCVHVTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRL TAVEDAVIGTPIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTLINQVKATTTAAFEN EDIPFERVVSALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLESVPVPSKAYTRFDM EFHLFQETDSLKGSVNFADELFKMETVENVVRVFFEILRNGLQSSRTPVSILPLTDGIVT LEKLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGWL RRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIV LIGHDTAPPDIEVINVEFVRIRDALNDSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGR PKGVMIEHRVIIRTVTSGCIPNYPSETRMAHMATIAFDGASYEIYSALLFGRTLVCVDYM TTLDARALKDVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDA QGLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGI GVMGELVVTGDGLARGYSDKALDENRFVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGR MDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQ-QNEDQAP-EILGFVVADHDHSEND IRGQRVELGAVETHLRQQMPDDMTIVVEAVKFSDSSSTTVLTAFLIGAG-

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Weber G., Schoergendorfer K., Schneider-Scherzer E., Leitner E., "The peptide synthetase catalyzing cyclosporine production in Tolypocladium niveum is encoded by a giant 45.8-kilobase open reading
                                                                                                                                                                                                                                                                                                                      frame.";

Curr. Genet. 26:120-125(1994).

Curr. Genet. 26:120-125(1994).

Curr. Genet. 26:120-125(1994).

I FUNCTION: THE CONSTITUTE AMINO ACIDS OF CYCLOSPORINS ARE ACTIVATED AS AMIONACTULABENT WITH PEPTIDE BONDS FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER INTERMEDIATES.

ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.

I CONFACTOR: CONTAINS 11 COVALENTLY BONND PHOSPHOPANTETHEINES.

I PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF CYCLOSPORINS.

I SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.

EMBL: 228383; CAA82227.1;

HSSP: P14687; 1AMU
  EPLYDLAIAGEVEPDGAGLKVTVIAKTQLFGRKRVEHLLEEVSKTFEGLNSSL
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Thu Jun

1379 NRNRPELEDIIGCFVNTC 						1797 FFREHVNAASHVISSSQD   :  12898 FSDHRIN		1898 PEQQLVGIGVMGELVVTG 	1958 GLIEFFGRMDTQFKIRGN                     13057 YQIEFFGRLDQQIKIRGH		2078 WLGETTRTLHDNRSLGNV    :              1 13175 WLNDTMRSLLDNQPPGKV		2196 FFGDVRSQATNEHFLAAR      :         13295 FFGDMRTYATNKDFLVAR		2308 ANQLNOKSLGDLIKSSDA :::::    : 13415 GTRMDRQALLQDLQDRQF	2358 STIRSSAEGDSSLSVPDI   :   :    :   13474 SRTQSRAKECPALSVADI	2412 RTLVNFPTDHHLRGSDLI
64 G	Qy	Qy	oy Db	QQ QQ	QY Db	Qy Dp	QY Db	QY	QY	δ Op	Qy	QQ .	Qy Db	Qy Db	oy Op	QY	Qy
PHOSPHOPANTETHEINE (POTENTIAL). PHOSPHOPANTETHEINE (POTENTIAL). PHOSPHOPANTETHEINE (POTENTIAL). 89051 MW: E26DA7AA35324C05 CRC64; 0%; Score 5000; DB 3; Length 15281; 4%; Pred. No. 1.2e-299;	CIHHEMLKAV	Qy 542 AIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVALTS 595 11640 ELVGVLAPRSCETIIAFLGIIKANLAYLPLDVNAPAGRIETILSSLPGNRLILLGSDTQA 11699	Qy 596 -KLHRETVQKLVGRCVVVDDELLQSVS-ASDDFSSLTKSQDLAYVIFTSGSTGDPKGIMI 653	QY 654 EHRAFSSCALKFGASLGINSDTRALQFGTHAFGACLLEIMTTLINGGCV 702	OY 703 CIPSDDRMNSIPSFINRYNVNWMMATPSYMGTFSPEDVPGLATLVLVGEQMSSSVN 759  11807 DYYTTID-IKALEAVFKQHHIRGAMLPPALLKQCLVSAPTMISSLEILFAAGDRLSSQ-D 11864	OY 760 AIWAPKLQLLNGYGQSESSSICFASNM-STEPNNMGRAVGAHSWVIDPNDIN 810	QY 811 RLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLYR 864	OY 865 TGDLARY-ASDGSIVCLGRIDSQVKIRGQRVELGAIETHL-RQQMPDDLTIVVEATKRSQ 922	OY 923SANSTSLIAFLIGSSYFGNRPSDAHILDHDATKAINIKLEQVL 965    Db 12029 PELVAFFSLKGNANGTNGVNGVSDQEKIDGDEQHALLMENKIRHNLQALL 12078	IDRRR         IDRNE	OY 1026 KLHSIWVQSLGIDPATVNVGATFFELGGNSITAIKM-VNMARSVGMDLKVSNIYQH 1080 : : :   :	QY 1081 PTLAGISAVVKGDPLSYTLIPRSTHEGPVEQSYSQGRLWFLDQLDVGSLWYLIPYAVRMR 1140   1:1 :	Qy 1141 GPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEV 1200	1201 LNOEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHISDGWSIDVLRRDLNOLYSAAL   :	QY 1261 KDSKDPLSALTPLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSPAKIPTDFARPA 1318	Qy 1319 LLSGDACCVHVIDGELYQSLRAFCNEHNTISFVVLLAAFRAAHYRLTAVEDAVIGTPIA 1378 	

--ITLLPPALLKQCL------ADAPSVLSSLESLYIGGDRL 12937 ARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRF 2255 |||:|||| ||:| |||:||:||| |||| ||:| |ARAVHTLGSNASKAMVRQQVAKLEDDEEELLVDPAFFTSLSDQF 13354 2RGDDVVAVSNIPYSKTIMERHLSQSLDDDEDGTSAVDGTAW-I 13473 QCMRINIDHHDTFGTLINQVKATTTAAFENEDIPFERVVSALQ 1438 1557 /LKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDI 1676 RMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALKDV 1796 AVHSQKDLGRFKFQGLESVPVPSKAYTRFDMEFHLFQETDSLKG 1498 SNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVI 1736 INRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVVADH 2017 WVLEIGTGSGMILFNLD--SRLESYVGLEPSRSAAAFVNKATES 2135 DOVPLRVPRRLSRTLMFFFLVVTDSTAPDALDA-QGLYQG---- 1851 'NGYGPTENGVMSTIYPIDSTESFINGVPIGRALN-NSGAYVVD 1897 VQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHE 2077 NELSAYRYAAVVHVRGSL----GDE----LVLPVEKDDWIDFQ 2307 DAA--IMAVSKIPFEITAFERQVVASLNSNID------EWQL 2357 JIFRIAGEAGFRVEVSSARQWSQNGALDAVFH-----HCCSQG 2411 LITNRPLORLONRRIAIEVRERLRSLLPSYMIPSNIVVLDKMPL 2471 VVRVFFEILRNGLQSSRTPVSILPLTDGIVTLEKLDVLNVKHV-

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2454 LPSYMIPSNIVVLDKMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCEE 2513
                                                                                                                                                            2514 ATEVFGMKVDITDHFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIRQ 2573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             968 HSIPSFYICMLELPRTATGKIDR----RRLRIMGKDILDKQTQGAIVQQAPAPIPV---F 1020
 GDQEPEMIGFVVVRADETVQQDLSRTHGAVNSANWEEQFEI----QTEKEIRNRLQNLLPS 163
                                                                                                                   ONGALDAVFHHCCSQG -- RTLVNFPTDHHLRGSDLLTNRPLQRLQNRRIAIEVRERLRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPNDINRLVPIGAVGELVIESPGIARDYIVPPPPEKSPFFTDIPSWYPANTFPDGAKLYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              865 TGDLARY-ASDGSIVCLGRIDSQVKIRGQRVELGAIE-THLRQQMPDDLTIVVEATKRSQ
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Chaetosphaeriaceae; mitosporic Chaetosphaeriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bernhard F.; Identification of genes encoding for peptide synthetases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1051 1051
1051 AA; 116526 MW; 7CB926576B2F0619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; X96559; CAA65395.1; -. HSSP; P14687; lAMU.
                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR00380; Pantne_attach.
InterPro; IPR00380; Pantne_attach.
InterPro; IPR00380; Pantne_attach.
InterPro; IPR00301; AMP-binding; 2.
Pfam; PF00560; pp-binding; 1.
PRINTS; PR00154; AMPBINDING.
PROSITE; PS00455; ACP_DOMAIN; 1.
PROSITE; PS00012; PHOÇPHOPANTETHEINE; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.5%; Score 2496; DB 3 llarity 47.8%; Pred. No. 5e-146; Conservative 185; Mismatches 30
                                                                                                                                                                                                                  GLGLQQPVSDGQG-QDRSAHMAPRTETE 2600
                                                                                                                                                                                                                                 1051
                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   negative bacteria and filamentous
                                                                                                                                                                                                                                                                                                                                                                                       Peptolide synthetase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                       Cylindrotrichum oliqospermum.
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                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=NRRL 18230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=72418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cylindrotrichum
                                                                                                                                                                                                                                                                                                                                                01-MAY-1997
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                           1632 GVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALN 1691
                                                                                                                                                                                                                                                                                                                                                                                                    DSNADGFEVIEHDSTKPSATSLAYVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSE 1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1752 TRMAHMATIAFDGASYEIYSALLFGRTLVCVDYMTTLDARALKDVFFREHVNAASHVTSS 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRDAAVVLQ--QNEDQAPEILGFVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIG-E 2048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 VIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVRSQATNEHFLAARAIHTLG--KNATKDD 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLK-SSDAAIMAVSKIPFEITAFERQVV 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2346 ASLNSNIDE-------WQLSTIRSSAEGDSSLSVPDIFRIAGEAGFRVEVSSARQWS 2395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSS 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1812 SQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDAQGLYQGVQCYNGYGPTENGVMSTIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1872 IDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDKALDENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRILHDNRSLGNVLEIGTGSGMILFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2227 VRQKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELSAYRYAAVVHV
'Highly conserved n-methyltransferases as an integral part of peptide
                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                     Length 983;
                                                                           Burmester J.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 248743; CAA88634.2; -
R EMBL; 248743; CAA88634.2; -
R InterPro; IPR000873; AMP-bind.
R Pfam; PF00501; AMP-bind.
R Pfam; PF00550; pp-binding; 1.
R Pfam; PF00550; pp-binding; 1.
R PROSITE; PS50075; ACP-DOMAIN; 1.
R PROSITE; PS00012; AMP-BINDING; 1.
R PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                         109069 MW; 1784588502EE7CBD CRC64;
                                                                                                                                                                                                                                                                                                   ilarity 58.7%; Pred. No. 2.1e-169; Conservative 153; Mismatches 225;
                                                                                                                                                                                                                                                                                    17.8%; Score 2871; DB 3; 58.7%; Pred. No. 2.1e-169;
                         Biochem. Mol. Biol. Int. 37:201-207(1995)
                                                                                                                                                                                                                                                       983 AA;
                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 580; Conserv
                                                      SEQUENCE FROM N.A. STRAIN-BBA 63933;
             synthetases
                                                                                                                                                                                                                                           NON_TER
SEQUENCE
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                                                                                                         Schauwecker F., Pfennig F., Grammel N., Keller U.;
"Construction and in vitro analysis of a new bi-modular polypeptide synthetase for synthesis of N-methylated acyl peptides.";
Chem. Biol. 77:287-297(2000).
EMBL; AF204401; AAF42473.1;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1899;
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                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0154; AMPEDINDING.
PROSITE; PS50075; ACP_DOMAIN; 3.
PROSITE; PS00455; AMP_BINDING; 3.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_3.
                                                                                                                                                                                                                  InterPro; IPR001601; Methyltransf.
InterPro; IPR001880; Ppantne_attach.
InterPro; IPR000051; SAM_bind.
InterPro; IPR001031; Thioesterase.
Pfan; PF00501; AMP-binding; 3.
Pfan; PF00668; Condensation; 3.
Pfan; PF00550; pp-binding; 3.
Pfam; PF00550; Thioesterase; 1.
                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 11523;
MEDLINE-20243879; Pubmed-10780924;
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InterPro; IPR001242; Condensa
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                                                                                            .080 HPTLAGISAVVKGDPLSYTLIPKSTHEGPVEQSYSQGRLWFLDQLDVGSLWYLIPYAVRM 1139
                                                                                                                                                RGPVNVDALRRALAALEQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDP-- 1197
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DR HSSP; P14687; 1AMU.  DR InterPro; IPR001206; AATRNA_ligaseII.  DR InterPro; IPR001242; Condensatn.  DR InterPro; IPR001242; Condensatn.  DR InterPro; IPR001201; Erythcrurin.  DR InterPro; IPR001801; Methyltransf.  DR InterPro; IPR001801; SAM_bind.  DR InterPro; IPR000051; SAM_bind.  DR InterPro; IPR000051; SAM_bind.  DR InterPro; IPR0010379; Ser_estrs_site.  DR Pfam; PF005601; AMP-binding; 4.  DR Pfam; PF00668; Condensation; 5.  DR Pfam; PF00668; AMP-binding; 4.  DR Pfam; PF00975; Thioesterase; 1.  DR Pfam; PR00134; AMPBINDING.	PRINTS; PRO0611; ERYTHCRUORIN. PROSTTE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1. PROSTTE; PS00455; AMP_BINDING; 4. PROSITE; PS00455; AMP_BINDING; 4. PROSTTE; PS00412; PHOSPHOPANTETHEINE; UNKNOWN_4. PROSTTE; PS004012; PHOSPHOPANTETHEINE; Length 4848; BEST Local Similarity 26.7%; Pred. No. 4.5e-131; Matches 877; Conservative 474; Mismatches 1280; Indels 659; Gaps 72 GHAVYDVPTDIDISRFALAWKEIVNOTPALRAFAFTSDSGKTSQVILKDSFV	DD 31 GPDVTYQMVFELRGPLDEDGLRAAAAALLKRHPNLRAGFWQQGVERPVQFV 82  QY 124 FSWMCWSSSSPDEVVRDEAAAAS	Qy         367 GDNGSAACDFQTVLLVTDGSHVNNGINGFLQQTTESSHFMPCNNRALLLHC 417           Db         344 TGTGELFDTVVVFENYPLDPAVLRAEARGLRLAGFEVSDATHY-PLSLLAI 393           Qy         418 QMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVN 467           1         1   1   1   1   1   1   1   1   1   1
2614 -QVGITDNFFDLGGHSLMATKLAVRICHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKT 26 :	2607 AAPRLIVTPTSEADLPDALEAAARYAFD-LAEGPPL-RTELFELSARE 265 2837 RVIMRISHALY-DGLSLEHVVRKLHMLYNGRSLLPPHQFSRYMQYTADGRESGHGFWRDV 289 1	Qy         2976 PVEYQDIVGECTNAVPRAHIESS-DYNQLLHDIQDQYLLSLPHETIGFSDLKRNCTDWP 3034           Db         2813 ALD01:1   1   1   1   1   1   1   1   1   1	GN STREPDE.  OS Streptomyces pristinaespiralis.  OC Actinobacteria; Actinobacteridae;  OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  OX NCBL_TaxID=38300;  RN [1]  RP SEQUENCE FROM N.A.  STRAIN=SP92;  RA Grecy-Lagard V.A., Saurin W., Thibaut D., Gil P., Naudin L.,  ROUGET J., Blanc V.;  RN Crouzet J., Blanc V.;  RN Crouzet J., Blanc V.;  RN [2]  RN [2]  RN SEQUENCE FROM N.A.  STRAIN=SP92;  RX MEDLINE-9715864; Pubmed=9006024;  RX MEDLINE-9715864; Pubmed=9006024;  RX MEDLINE-9715864; Pubmed=9006024;  RY Pristinamycin I biosynthesis in Streptomyces pristinaespiralis:  RT "Pristinamycin I biosynthesis in Streptomyces pristinaespiralis:  RT "Pristinamycin I biosynthesis in Streptomyces pristinaespiralis:  RY "Pristinamycin I biosynthesis in Streptomyces pristinaespiralis:  RY "Pristinamycin I biosynthesis in Streptomyces pristinaespiralis:  RY "Pristinamycin I biosynthesis in Streptomyces Protection of the first two structural peptide  RY Synthetase genes.";  SHL J. Bacteriol: 179:705-713(1997).  EMBL; X11548; CAA72312.1;  BNB EMBL; X98690; CAA67249.1;

103 CIPSODDRANSIDSFINRYNO	725	803 784	859 832	917.	977	1035 985	1094 . 1033	1148 1092	1195	1255	1308 1255	1366 1315	1426 1375	1483 1431	1537 1491	1597	1657	1716
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1768 GDATAPD--QAARFAPGRRWVNAYGLTETTVCATM---SEPATGDGAPPIGRPVAHARV 1821 :: :: | |: |: || |: || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || | 2386 LYTSGSTGRPKGVMIEHRVIIRTVTSGCIP-NYPSETRMAHMATIAFDGASYEIYSALLF 1775 GRTLVCVDYMTTLDARALKDVFFREHVNAASHVTSSSQDVP-LRVPRRLSRTLMFFFLVV 1834 1714 GAGLVLADADDLLPGPSLARLVHDRHITLIALPPSALPALPDGALPPGTD-----LIVA 1767 1835 TDSTAPDALDAQGLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGV-PIGRALNNSGA 1893 YVVDPEQQLVGIGVMGELVVTGDGLARGYSDK-ALDENRFV----HITVNDQTVKAYRTG 1948 DRVRYRIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPE 2008 2009 ILGFVVAD-HDHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPS-TIGSDFKGWTSMYD 2066 2067 GSQIDFDEMHEWLGETTRTLHDNRSLG----NVLEIGTGSGMILFNLDSRLESYVGLEPS 2122 :| :| || : | 1 |: |
1996 AEEIPLEEMREWRAATV----DRVLALRPRRVLEIGCGTGLILSQVAPHTEEYRGTDLS 2050 AEIADTLIHL--PNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDM 2237 EEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLP 2297 2298 VEKDDWIDFQANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAFERQVVASLNSNIDEWQL 2357 STIRSSAEGDSSLSVP-----DIFRIAGEAGFRVEVSSARQWSQNGALDAVFHHCC 2408 2409 SQG-----RTLVNFPTDHHLRGSDLLTNRPLQRLQNRRIAIEVRERLRSLLPSYMIPSNI 2463 VVLDKMPLNANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCEEATEVFGMKVD 2523 2524 ITDHFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIRQGLGLQQPVSD 2583 2386 2584 GOGODRSAHMAPRIETEAILCDEFAKVLGF-QVGITDNFFDLGGHSLMATKLAVRIGHRL 2642 2643 DTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEIVGGREMAEYSPFQLLFTEDPEEFMASE 2702 -----AQE 2472 2703 IKPQLELQEIIQDIYPSTQMQKAFLFDHTTARPRFYPFYIDFPSTSEPDAAGLIKACES 2762 2473 ARPPLTARTRPAEV-PLSFAQYRLWFLHRMEGPGPTYNIPMSLRLTGTLDTAALRAALAD 2531 |::||::||:||:||:||
VLLDRLPLSANGKLDR---------DALPAP----GAELAVRDLFQAPTVAALAERVDG------2238 1894 1949 1882 2180 2108 2358 2464 2365 2387 2387 2446 1717 O.Y g q δy Db Qy Db Qy a y δŽ ò άqα do y ρp Db Dy 9 & 9 42 42 43 2y Ob à

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LOATFLGHDPYLAGADGVPPGDAKLRTTLTAPFTFDASMEQL 1013
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                                                                                                             91;
                                                                                                                                        OHLMVPNPTTTAE--HRITFPLSQKALS-----NSAIC 283
                                                                                                                                                                                                                                                                                                                                                                                                                             TLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVH 531
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                                                                                                                                                                                                           EALFGAVTEQSLPFDKHYLADGTYQTVAPLRVHCQSNLRASD 340
                                                                                                                                                                                                                                                                       --PF----GLRDIRNTGDNGSAACDFQTVLLVTDGSH---- 387
                                                                                                                                                                                                                                                                                                                                                           SLDIKRADDGSY-----RGILNYCPDLFDRRRME----VLV 759
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                                                                                                                                                            DIVVGVPAAGRIRTETEPLV-GFFVNTLPLRAICAPGLSFRD 653
                                                                                                                                                                                                                                                                                             -DHNVIDSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTE 471
                                                                                                                                                                                                                                                                                                                                       ---LQQITESSHFMPCNNRALLLHC-----QMESSGALLV 427
                                                                         Score 2146.5; DB 2; Length 2841;
Pred. No. 1.8e-123;
94; Mismatches 1025; Indels 357; Gaps
                                             MW; F4F81106BB756037 CRC64;
ANCHORING; UNKNOWN_1.
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ANQLNQKSLGDLLKSSDAAIMAVSKIPFEITAFERQVVASLNSNIDEWQLSTIRSSAEGD 2367
                                                                                                                                                                                                                                                                            2590 VHDLASLSARLGRGGPDALLV-----RGVANDRLTRDNELLDAPARTTA--- 2633
                                                                                                                                                  TSLKDRFPGLVEHVEILPKNMEAVNELSAYRYAAVVHVRGSLGDELVLP-VEKDDWIDFQ 2307
  LPNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAELEDMEEELLVEPAFF
                                                                                        InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR001601; Methyltransf.
InterPro; IPR003880; Ppantne_attach.
InterPro; IPR000051; SAM_bind.
Pf005051; AMP-binding; 4.
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--GDPLSYTLIPKSTHEGPVEQSYSQGRLWFLDQLDVGSLWYLIPYAVRMRGPVN 1144
                                                                                                                                                                                                                                                                                                                                                                                HPRPAVQSQRGETVEFPLPAPLVARLEALCREQGVTLFMALFGAFQVLLARYSGQDDVVV 1681
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SDLLTNRPLQRLQNRR---IAIEVRERLRSLLPSYMIPSNIVVLDKMPLNANGKVDRKEL 2482
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SSLSVPDIFRIAGEAGFRVEVSSARQWSQNGALDA - - VFHHCCSQGRTLVNFPTDHHLRG
                                                                                                                                                       --VEPEDLWGLADSTPYRVSVSWAAA-DPRGAMDVLLVRRDAHDDGPLLYPHPVP---EP
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Racteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
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Rouhiainen L., Paulin L., Suomalainen S., Hyytiainen
Haselkorn R., Sivonen K.;
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EMBL: A.7356555; CACO1604.1; -.
HSSP; P14687; 1AMU.
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llarity 25.1%; Pred, No. 1.3e-120;
Conservative 500; Mismatches 1065;
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PRINTS; PR00154; AMPBINDING.
PROSITE; PS00075; ACP_DOMAIN; 4.
PROSITE; PS000155; PHOSPHOPANTETHEINE; UNKNOWN_2.
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QY 927 937  Db 3174 QARACIEKLGLADKITVIHGDATLVDIPELADVCVSEIVGAIGGSEGAAVIINNARRFLK 3233	QY 938 942   1   1   1   1   1   1   1   1   1   1	Qy 943ILDH 951  DD 3294 NVLSTVDVLEDLNFNEYISPEFSHEVQLEIHKNGRMNGFLVWLNLHTIAGEEIDILEHEY 3353	QY 952 957   : 1; Db 3354 CWLPVYLPLFEPGIEVEYGDVIQAVCSRTLCENNLNPDYAIKGRLLKKNGENINFEYVSY 3413	QY 958	OY 984 ATCKIDRRRLRIMGKDILDKOTOGAIVQOAPAPIPVFADTAAKLHSIWVOSLGIDPAT 1041	OY 1042 VNVGATFFELGGNSITAIKMVN-MARSVGMDLKVSNIYQHPTLAGISAVVKGDPL 1095 1 :	QY 1096 SYTLIPKSTHEGPVEQSYSQCRLWFLDQLDVGSLWYLIPYAVRMRGPVNVDALRRALAAL 1155  1	QY 1156 EQRHETLRTTFEDQDGVGVQIVHEKLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNL 1211	QY 1212 SSEAGWRATLLRLGEDDHILTIVMHHIISDGWSIDVLRRDLNOLYSAALKDSKDPLSALT 1271  ::::    :::  ::  ::    ::   Db 3699 ANGSVLRVKLWQVAPDEYVLLLAIHHIAADGWSMGILIDELSAYYRSFSTGSSVELPELS 3758	QY 1272 PLPIQYSDFAKWQKDQFIEQEKQLNYWKKQLKDSSP-AKIPTDFARPALLSGDAGCVH 1328  [  :	QY 1329 VTIDGELYQSLRAFCNEHNTTSFVVLLAAFRAAHYRLTAVEDAVIGTPIANRNRPELEDI 1388 :: :	OY 1389 IGCEVNTQCMRINIDHHDTFGTLINOVKATTTAAFENEDIPFERVVSALOPGSRDLSSTP 1448                :  :  :	QY 1449 LAQLIFAVHSQKDLGRFKFQGLESVPVPSKA-YTRFDMEFHLFQETDSLKGSVNFADELF 1507	QY 1508 KMETVENVVRVFFELLRNGLQSSRTPVSILP-LTDGIVTLEKLDVLNVKHVDXPRES 1563   : ::   :   :   :	QY 1564 SLADVFQTQVSAYPDSLAVVDSSCRLTYTELDRQSDILAGMLRRRSMPAETLVAVFAPRS 1623 : : :     :     :     :	Qy 1624 CEȚIVAFEGVLKANLAYLPLDVRSPSARVQDILSGLSGPTIVLIGHDTAPPD 1675	1676 IEVTNVEFVRIRDALNDSNADGFEVIEHDSTRPSATSLAYVLYTSGSTGRPKGVMIEHRV	Db 4170 LDEIWQQIAQNSQENLTGIVIAANLANTYTSGSTGKPKGWKEHQ 4216
57 LDMIDCNALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPALRAFTSDS 110	GKTSQVILKDSFVFSWMCWSSSSSPDEVVRDEAAAAASGPRCNRF	SSDAT	DTDSQSVSVVSMSCEDNAVSATHFWQTHLNDLNASVFPHLSDHLMVPN	PTTAEHRITFPLSQKALSNSAICRTALSILLSRYTHSDEALFGAV	TEQSLPEDKHYLADGTYQTVAPLRYHCQSNLRASDVMDAISSYDDRLGHL	APF        ODLPFEM	NNRALLLHCQMESSGALLVAYYDHNVIDSLQTTRLLQQFGHLIK-CLQSPLDLSSMAE  THE STATE	VNLMTEYDRAEIESWNSQPLEV-QDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNV :   :	SSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIASMLAVLKSGNAFTLIDPNDPPARTAQVV :::   :::   :   :  :       :  :       :  :	TOTRATVALTSKLHRETVQKLVGR~~CVVVDDELLQSVSASDDFSSLTKSQDLAYVI ::      ::     :    :    :    :      :  :	640 FTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSDTRALOFGTHAFGACLLEIMTTL 696	INGGCVCIPSDDDRMNSIPSFINEYNVNMMATPSYMGTESPEDVP   I	-GLATIVIAGEOMSSSVNAIWAPKLOLLNGYGOSESS-SICFASNMSTEPN     :       :   : : : : : : : : : : :	NMGRAVG-AHSWVIDPNDINRLVPIGAVGELVIESPGIARDXIVPPPPEKSPFFTDIPSW	YPANTEPDGAK - LYRTGDLARYASDGSIVCLGRIDSQVKIRGQRVELGAIFHL SIDERANGEDTI VASTATATATATATATATATATATATATATATATATATAT	;	3054 VREVVVVARSDQPDNKRLVAYVVPQQKNLESSKKPEKLSTDKVELWPSIAEYYVYDDLLY 3113	YAMTNDHRRNDSYKVAINOLVKDKIVVEIGTGKDAILSRFCVQGGANKIYAIERNEETCR

음 δ Pb ò g ŏ g δý g δ g δ g ò g Qγ Pb δ g ö g δ q δ g ŏ g Qγ q

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GL-GQDSYFIWSVHHALYDGWSQNLLFERVKQLY------MGDAISKSPSYNR 2355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2356 FIHFLAQEDTKSANKFWKSQLLREQAPTSFP-----VLPSPSYKPRADHVQTLRLPLSR 2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2470 ELPS--RNTTVYKYLELVQNQAMEMMPYEHVGIQSLRR-----LCLEAEPDYELDLKH 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K---ALSNSAICRTALSILLSRYTHSDEALFG-AVTEQSLPFDKHYLADGTYQTVAPLRV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRAFAFTSDSGKTSQVILKDSFVFSWMCWSSSSSPDEVV-RDEAAAAASGPRCNRFVLLE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 DMQTKKCQLVWTFSHALVDVTFQQRVLSRVFAAYKHEKDTHRPETPESSDATDTDSQSVS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLLVTDGSHVNNGINGFLQ---QITESSHFMPCNNRALLLHCQMESSGALLVAYYDHNVI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSLQTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEYDRAEIESWNSQPLEVQDTLIHHE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 LDSSRIEAIKPCTPFQLDMIDCNALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 MLKAVSHSPTKT-AIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWV 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 IASMLAVLKSGNAFTLIDPNDPPARTAQVVTQTRATVALTSKLHRETVQKLVGRCVVVDD 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRTRVILTNINSV-QVVLRQE-----NPWKEGLTLESYLEKDNGLPIEYGGLLHRLCIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 VVSMSCEDNAVSATHFWQTH-LNDLNASVFPHLSDHLMVPNPT--TTAEH--RITFPLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 HCQSNLRASDVMDAISSYDDRLGHLAPF---GLRDIRNTGDNGSAAC------DFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patterson I.C., Charnley A.K.,
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                                                           MEDLINE=97082966; PubMed=8964498; Bailey A.M., Kershaw M.J., Hunt B.A., Patterson I.C., Charnley A. Reynolds S.E., Clarkson J.M.; Reloning and sequence analysis of an intron containing domain of peptide synthetase from the entomopathogenic fungus Metarhizium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711;
                                                                                                                                                                                                                                                                        Bailey A.M., Reynolds S.E., Charnley A.K., Clarkson J.M.;
"Evidence for multiple peptide synthetases from Metarhizium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.5%; Score 2018.5; DB 3; Length Best Local Similarity 23.9%; Pred. No. 4.9e-115; Matches 795; Conservative 536; Mismatches 1278; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5157 AA; 573954 MW; 1038242BA3143868 CRC64;
                                                                                                                                                                                                                                                                                                               anisopliae.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X89442; CAA61605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                     nassi; kranos; lamu.
InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR001280; Ppantne_attach.
Pfam; PF00050; Pp-binding; 4.
Pfam; PF00050; pp-binding; 4.
PROSTITE; PS00075; AMPBINDING.
PROSTITE; PS00075; AMP_BINDING; 4.
PROSTITE; PS00075; AMP_BINDING; 4.
PROSTITE; PS00012; PHOSPHOPANTETHEINE; UN
Phosphopantetheine.
SEQUENCE 5157 AA; 573954 MW; 1038242)
                                                                                                                                                                                       Gene 173:195-197(1996).
                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN=ME1;
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                                                                                                                                                                                                                                   VMGELVVTGDGLARGYSDK-ALDENRFVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGR 1965
                                                                                                                                                                                                                                                                                                                                                                                                2026 Q-----SANQVEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMH 2076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVDITDHFFNLGGHSLLATKLISRIDQRLKVRITVKDVFDHPVFADLASVIRQGLGLQQ 2579
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.
NCBL_TaxID=5530;
                                                             ----RALKDVFFREHVNAASHVTSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDAQ
                                                                                       GLYQGVQCYNGYGPTENGVMSTIYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIG
                                                                                                                                                                          S--AGRNFFNAYGPTEGSVCAT---LAKCSALTOKLPLVGPIANVQVYILDSQLQPVPIG
                                                                                                                                                                                                                                                         QVLPEQLAQWQGEYVSDWQKLYEQSYSQQQTPTDDPTF -- NISGWNSSYTGKAIPDSEMR
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                                                                                                                                                                                                                                                                                                             MDTQFKIRGNRIESAEIEAALLRDSSVRDAAVVLQQNEDQAPEILGFVVADHDHSENDKG
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Last annotation update)
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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949 TVQRVLELAPDVDIARFQAAWETTARCTPIMRTRIVQHVELGLLQAVVDED---IEWKTL 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGLVSARHATTVFGPGWATLEVSRRALSSMPEGPLGQVDASS---; LAWVIFTSGST 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSSSSPDEVVRDEAAAAASGPRCNRFVLLEDMQT --- KKCQLVWTFSHALVDVTFQQRVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 APF---GLRDIRNTGDNGSAACDFQTVLLVTDGSHVNNGINGFLQQITESSHFMPCNNRA 412
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                                                                                                                                                                               12 DLPPTPASFCSHGDSPLNSSYEQLFHLYGL-DSSRIEAIKPCTPFQLDMIDCNALDKQSA
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                                                                                                                                                                                                                                             71 IGHAVYDVPTDIDISRFALAWKEIVNQTPALRA-FAFTSDSGKTSQVILKDSFVFSWMCW
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                                                                                                                Length 4360;
                                                                                                                                                  Indels
                                                                                 4360 AA; 479036 MW; A5172C653CEBA468 CRC64;
                                                                                                                                                  Conservative 567; Mismatches 1430;
                                                                                                                Score 2002; DB 3;
Pred. No. 3.8e-114;
PROSITE; PS50075; ACP_DOMAIN; 4.
PROSITE; PS00455; AMP_BINDING; 3.
PROSITE; PS00013; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_4.
PROSIPE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_4.
SEQUENCE 4360 AA; 479036 MW; A5172C653CEBA46
                                                                                                                12.4%; Score 2002;
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                                                                                                                                                                                                                                                                                                                                           INTATNE-----FLDEFAKEPVRLGHPLIRFTIIKQTKSMRVIMRISHALYDGLSLEHVV 2856
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                                                                                                                                                                             GKTRVSFAYNRRMHHQDLIRQWVSESKECLGTLTSRLSVTELQLTRSSFPLLSLEDRE-- 4757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson R.D., Johnson L., Itoh Y., Kodama M., Otani H., Kohmoto K.; "Cloning and Characterization of a Cyclic Peptide Synthetase Gene from Alternaria alternata Apple Pathotype Whose Product Is Involved in AMTOXIN Synthesis and Pathogenicity.";
                CDEFAKVLGFQVGITDNFFDLGGHSL
                                               4595 PLHVPVMEEEDELKILAHTKDLRRQVPSSGYPYFCSRFLSPOGOOT----FGHH--
                                                                               MATKLAVRIGH------RLDTTVSVKDVFDHPV-------LFQLAIALDNLVQ
                                                                                                    --TRMEVILNYQGRYQQLERDDALLRPEPLAENEVHKDQGSDMHRFSLFEISV---EVVQ
                                                                                                                                                -----SPFQLLFTEDPEEF
                                                                                                                                                                                                           2699 MASEIKPQLELQEI----IQDIYPSTQMQKAFLFDHTTARPRPFVP----FY--IDF
                                                                                                                                                                                                                              PSTSEPDAAGLIKACESLVNHLDIFRTVFAEA---SGELYQVVLSCLDLPIQVIE-TEDN
                                                                                                                                                                                                                                                                                                                                                               :: :|||| ||| || :|: 1871 VSEKMRSQEMIGFL----EPV----PHHRLAIFTTASKVMCCLDISHALTDGMSMRLLM
                                                                                                                                                                                                                                                                                                                                                                                                          RKLHMLYNGR-SLLPPHQFSRYMQYTADGRESGHG-FWRDVIQNTPMTIL--SDDTVVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                          RDLYMAYESNLQLAPGPMYSDY1AFLQQQPASQDA1FWRQYLDAVKPCHLPRPDAPLCSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDATCKALHLSKIVNIPSQVLRGSSNI--ITQATVFNAACALVLSRESDSKDVVFGRIVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4982 REQRSVHVHLKE----DFAQIQGFCKTYGLIVANLIQSTWGLVLRKYTGCDDAVFGYLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria
NCBI_TaxID=5599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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EMBL; AF184074; AAF01762.1; -.
HSSP; P14687; LAMU.
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InterPro; IPR001242; Condensatn.
InterPro; IPR001092; HiH_basic.
InterPro; IPR003880; Ppantne_attach.
Pfam; PF00501; AMP-binding; 5.
Pfam; PF00550; pp-binding; 4.
                                                                                                                                             SKTN-EIVGGREMAEY------
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01-MAY-2000 (TrEMBLre)
01-MAR-2002 (TrEMBLre)
AM-toxin synthetase.
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Q C	2359 SDGYSFSCRARFDSRVLSAQVAERMMAQLGHVVSQLVAVTASPSSS 2404	ò	2323 SDA
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Qy	1589 LTYTELDRQSDILAGWLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLPLDV 1645	Š	
qa	2465 CSYAQLEKLSDALAAMLTDLGIGLGLDQQLVPLCFERSMWVVVAMMAVLKTGAGIVPLDP 2524	qq	
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7 g	APDIATERIGITANG-CCICIPSDAERLERLPOECTTEAVWIAILTP	qa	3652 GDNI
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G qa	SVARLYTPNDIPTLRSLCLAGEAPNKODISTWOHRIPFLENCYGPAEA	qa	3692 PRT
ò	GVMSTIYPIDSTESFINGVPIGRAI.NNSGAVVVDPF001VGTGVMGELVVVTGDGTARG	Qy	2616 GITI
7 a		qa	3752 HLDI
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1922	2 YSDKALDENRFUHITVNDQTVKAYRTGDRVRYRIGDGLIEFGRMDTQF 1970   :
1971	1 KIRGNRIESABIEAALLRDSSVRDAAVULQQNEDQAPEILG 2011 
2012	2 EVVADHDHSENDKGQSANQVEGWQDHFESGMYSDIGEIDPSTIGSÖFKGWTSMYDG 2067 :
2068	SQIDFDEMHE :       RAVDAPHHQPQRLPSTVMEETLRDL
3023	6 LEIGLFNLDSRLESYV 2117
2118	8GLEPSRSAAAF-VNKATESIPSLAGKAKVQVGTATDIGQVDDL 2159
2160	0
3196	0 VRSQATNEHFLAARAIH2216 
325	7TLGKNATKDDVRQKMAELEDMEEELLVEPA
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227	0 BAVNELSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLKS 2322   1   1   1   1   1   1   1   1   1
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2367	67 DSSLSVPDIFRIAGEAGFRVEVSSARQWSQNGALDAVFHHCCSQGRTLV 2415 :
241 354	6 -NFPTDHHLRGSDLLTNRPLORLONRRIAIEVRERLRSLLPSYMIPSNIVVLDKMPL 2471
2472 3596	2 NANGKVDRKELSRRAKVVPKQQTAAPLPTFPISEVEVILCEEATEVFGMKVDITDH 2527 :   :     :     : :     : :       : :
365	B FFNLGGHSLLATKLIS   :: :  C GDNKSRPAICWSKDYG
2588	8 DRSAHFAKULGFOV 2615
261,375	6 GITDNFFDLGGHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAIALDNLVQSKTNEI 2675 :  :

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1240 SDGWSIDVLRRDLNQLYSAALKDSKDPLSALTPLPIQYSDFAKWQKDQFIEQE----- 1292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1180 KLSEEMKVIDLCGSDLDPFEVLNQEQTTPFNLSSEAGWRATLLRLGEDDHILTIVMHHII 1239
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                                                                                                                                                                                                                    431 DH--NVIDSLOTTRLLQQFGHLIKCLQSPLDLSSMAEVNLMTEYDRAE-IESWNSQPLEV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCVVVDDELLQSVSASDDFSSLTKSQDL-----AYVIFTSGSTGDPKGIMIEHRAFS 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLNGYGOSESSSICFASNMSTEPNNM-----GRAVGAHSWVIDPNDINRLVPIGAVGE 820
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                                                                                                                                                                                                                                                                                                          488 QDTLIHHEMLKAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVY 547
                                                                                                                                                                                                                                                                                                                                                    SDRTLPELFEEQAARTPRATALTFEGRTVDYADLNARANRLARRLAARGAGPERT-VALR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.3%; Score 1984; DB 2; Length 1997; Best Local Similarity 29.2%; Pred. No. 1.2e-113; Matches 618; Conservative 378; Mismatches 899; Indels 222;
                                                                                       214245 MW; E60CF59E5615B398 CRC64;
    UNKNOWN_1
  PS00343; GRAM_POS_ANCHORING;
PS00012; PHOSPHOPANTETHEINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2676 VGGREMAEYSPFQLL--FTEDP---EEFMASEIKPQLE-LQEIIQDIYPSTQMQKAFLFD
                                                                                     HTTARPRPFVPFYIDFPSTSEPDAAGLIKACESLVNHLDIFRTVFAEASGELYQVVLSCL
                                                                                                                                                                                                                  3917 KLKGRFVAETLGDGDEIEAAVERVVSADKADINITGCPMPQFIFLSKRSKTEGFQSKLII
                                                                                                                                                                                                                                                           2840 MRISHALYDGLSLEHVVRKLHMLY----NGRSL------LPP-HQFSRYM-
                                                                                                                                                                                                                                                                                                                                                -QYTADGRESGHGFWRDVIQ---NTPMTILSD--DTVVDGNDATCKALHLSKIVNIPSQV
                                                                                                                                                                                                                                                                                                                                                                                                                                   2933 LRGSSNIITQATVFNAACALVLSRESDSKDVVFGRIVSGRQGLPVEY---QDIVGPCTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2990 VPVRAHIESSDYNQ-----LLHDIQDQYLLSLPHETIGFSDLKRNCTD--WPEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFSCCITYHNF------EYHPESQFEQ-----QRVEMGVLTKFV---
                          DLP----IQVIETEDNINTATNEFLDEFAKEPVRLGHPLIRFTII-KQTK----SMRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Streptogramin B biosynthesis in Streptomyces pristinaespiralis and Streptomyces virginiae: molecular characterization of the last structural peptide synthase gene."; submitted (FBB-1997) to the EMBL/GenBank/DDBJ databases. HSSP; p14687; IAMU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycesacses; Streptomyces. NCBI_TaxID-1961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gil P., Naudin
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Last annotation update)
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de Crecy-Lagard V.A., Saurin W., Thibaut D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001843; AMP-bind.
InterPro; IPR001849; Condensatn.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001601; Methyltransf.
InterPro; IPR0008051; SAM_bind.
Pfam; PP00501; AMP-binding; 2.
Pfam; PP00668; Condensation; 1.
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PRINTS; PRO0154; AMPBINDING.
PROSITE; PS50075; ACP_DOMAIN; 1.
PROSITE; PS00455; AMP_BINDING; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2002 (TrEMBLrel. 20,
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                                                                                     2730
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340 DVMDAISSYDDRLGHLAPFGLRDI	 0y	10/3 NEWYENNANDARYU- DOMADARANDERARANEFUCEUF HALGENEGIKIAVIWS 1920	
321 FMT	ୟ 	2337 ITAFERQVVASLNSNIDEWQLSTIRSSAEGDSSLSVPDIFRIAGE-AGFRVEVSSARQWS 2395	yo f
264 LDYWKQLLKNAPTLLELPTDRPRPPIQTFRGEIQ	අ <sub>ධ</sub> :		qo
233	Oy	AYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQKSLGDLLKSSDAAIMAVSKIPFE	λõ
177 VDVTFQQRVLSRVFAAXKHEKDTHRPETP-ESS 	ος 	2217 TLGKNATKDDVRQKMAELEDMEEELLVEPAFFTSLKDRFPGLVEHVEILPKNMEAVNELS 2276	νος ·
152 IVDLSELPESEREIACQQLATTEANRPFD	₹ aa aa aa aa aa aa aa aa aa aa aa aa aa	2159 LHPDLVVLNSVIQYFPSSEXLAEIADTLIHLPNVQRIFFGDVRSQATNBHFLAARAIH 2216   :     :    ::   : ::    ::   :     ::   1697 GFFDTIVLNSVVQYFPNADYLADVLTGVLDLLAPG-GSVYIGDVRNHRLETFRTAVELR 1755	Oy Op
68 QSAIGHAYZDVPTDIDISRFALAWKETYNQTPALKA  :: : : :::     99 QAALKLHGKLNYVALEQSLNKIIDRHEALRT		2099 GTGSGMILFNLDSRLESYVGLEPSRSAAAFVNKATESIPSLAGKAKVQVGTATDIGQVDD 2158 1	Oy Ob
B DGRODLPPTPASFCSHGDSPLNSSYEQLFHLYGLDS 	ολ 	2042 MYSDIGEIDPSTIGSDFKGWTSMYDGSQIDFDEMHEWLGETTRTLHDNRSLGNVLEI 2098	oy da
Query Match Best Local S Matches 775		1985 ALLRDSSVRDAAVVLQQNEDQAPEILGFVVADHDHSENDKGQSANQVEGWQDHFESG 2041	Qy Db
	S S S S S S S S S S S S S S S S S S S	1926 -ALDENREVHITVNDQTVKAYRTGDRVRYRIGDGLIEFFGRMDTQFKIRGNRIESABIEA 1984 	Oy Dp
PROSTIE: PSSOO75; FF WIRELING: PROSTIE: PSSOO75; ACP_DOMAIN; 3. PROSTIE: PSSOO703; ALBEHYDE_BRIYDR_CYS; UNKNOW		1869 IYPIDSTESFINGVPIGRALNNSGAYVVDPEQQLVGIGVMGELVVTGDGLARGYSDK 1925	Oy Dp
		1809 TSSSQDVPLRVPRRLSRTLMFFFLVVTDSTAPDALDAQGLYQGVQCYNGYGPTENGVMST 1868   :	Qy
EMBL; AFZU48U3; AAFIV HSSP; P14687; 1AMU. InterPro; IPR002086; InterPro; IPR000873;		1754 MAHMATIAFDGASYEIYSALLFCRTLVCVDYMTTLDARALKDVFFREHVNAASHV 1808 :  - - - - - - - - -	Qy Dp
Holimann D.; Hevel J.M.; Moole K.E.; "Characterization of the nostopeptolide biosy; Nostoc sp. GSV224."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ	RT	1700 VIEHDSTKP-SATSLAVVLYTSGSTGRPKGVMIEHRVIIRTVTSGCIPNYPSETR 1753 :::	Qy Db
		1643 LDVRSPSARVQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFVRIRDALNDSNADGFE 1699 :	Qy Db
NOSC. NOSC. NOStoc sp. GSV224. Bacteria; Cyanobacteria; Nostocales; Nostocac	00 00 00 00 00 00 00 00 00 00 00 00 00	1583 VDSSCRLTYTELDRQSDILAGMLRRRSMPAETLVAVFAPRSCETIVAFFGVLKANLAYLP 1642 	Oy Dp
		1526 GLQSSRTPVSILPLIDGIVTLEKLDVLNVKHVDYPRESSLADVFQTQVSAYPDSLAV 1582 1081 VAADPDQPIGRVGILDPAEKHRILHTWN-DTSRPGADATWPELFQARAAEHPDAVAL 1136	Oy Dp
SUL RAH	A O O O	1472 SVPVPSK-AYTRPDMEFHLFQETDSLKGSVNFADELFKMETVENVVRVFFELLRN 1525	O.y
2440RAIALEVREKL 2450   1   1   1   1   1   1   1   1   1   1	λ a	1412 INQVKATTTAAFENEDIPFERVYSALQPGSRDLSSTPLAQLIFAVHSQKDLGRFKFQGLE 1471 :::     ::    :     :	Oy Dp
	Qy	1352 VVLLAAPRAAHYRLTAVEDAVIGTPIANRNRPELEDIIGCFVNTQCMRINIDHHDTFGTL 1411 :	Qy dQ

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DB 2; Length 3317;
113;
1091; Indels 917; Gaps 115;
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|: : | | | | :
LIRASVV--KLTEVEHALVLTIHHIV 209
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| | : : | | | : :
RT-NFRTINEQPVQVI-TDSLNLNVP 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic gene cluster of
                                                                                                                                                                                                                                             ceae; Nostoc.
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AC4565 CRC64;
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update)
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ITLLAAYDTLLYRYTGTEDILYGSPIANRDRSEI 1441 NOVKATTTAAFENEDIPFERVVSALOPGSRDLS 1445 VP-VPSKAYTRFDMEFHLFQETDSLKGSVNFAD 1504 TELDROSDILAGWLRRRSMPAETLVAVFAPRSC 1624 : || : | ||: : | ||: CEFILDDAALP--VLLTQQSLLESLPEHTAQVV 1737 SYEIYSALLFGRTLVCVDYMTTLD-ARALKDVF 1797 : |:| |: | :| | ALELYLPLINGAKVVVVGREVASDGARLLLEL- 1848 RRLSRTLMFFFLVVTDSTAPDALDAQGLYQGVQ 1853 ---SFING-----VPIGRALNNSGAYVVDPEQ 1900 | : :|: LTQEKFISNPFKRSRGAEEQGSRGETFNSD--R 2019 RIPVSILPLIDGIVILEKLDVLNVKHVDYPRESS 1564 VQDILSGLSGPTIVLIGHDTAPPDIEVTNVEFV 1684 SGLSTQQLGMKLLCGGEALPPQLAHQLLETGAQ 1901 : :| ||||| : |: || ARSAIASGAALRAIAPIGRPIANTQFYILDSHL 1961 LDENRFVH-------ITVNDQTVK 1943 VEGWQDHFESGMYSDIGEIDPSTIGSDFKGWTS 2063 SLGNVLEIGTGSGMILFNLDSRLESYVGLEPSR 2123 TDIGQVDDLHPDLVVLNSVIQYFPSSEYLAEIA 2183 AARAIHTLGKNATKDDVRQKMAELEDMEEELLV 2243 AVNELSAYRYAAVVHVRGSLGDELVLPVEKDDW 2303 SKIPFEITAFERQVVASLNSNIDEWQLSTIRSS 2363 ARQWSQNGALDAVFHHCCSQGRTLVNFPTDHHL 2423 2100 g us-09-482-788-2.rspt

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325
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                                                                                                                                                                                                                                                                                                                                                                          101 KIFAITDRPFNLEKDSILRVNLFT----RSKKEHILLLTMHHIAGDMWSFDLLLSEFQTL 156
                                                                                                                                                                                                                                                                               IDISRFALAWKEIVNQTPALRAFAFTSDSGKTSQVILKDSFVFSWMCWSSSSSPDEVVRD
                                                                                                                                                                                                                                                                                                                                                                                                         YKHEKDTHRPETPESSDATDTDSQSVSVVSMSCEDNAVSAT-----HFWQTHLNDLNAS
                                                                                                                                                                                                                                                                                                                                                                                                                            247 VFPHLSDHLMVPNP-----TTTAEHRITFPLSQKALSNSA----ICRTALSILLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELPILNLFADKPRPPVQTYQGTGYSLKLDERLIQKLKYLALASGTSLYQVLLAAFYVLLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAVSHSPTKTAIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIIPVYFEKSKWVIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTALFNOLASVVPQAFSSLRYLLFGGE----AVDPKWVLEVLDKGAPQ-HLLHVYGPTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 TVREAQKHQD----YPFSLLAEQLQPQRDI-----SRSPLCQ----VSFTWQAHRWCEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYTHSDEALFGAVTEQSLPFDKHYLAD ----GTYQTVAPLRVHCQSNLRASDVMDAIS-
                                                                                                                                                                                   089F97BFC598EA84 CRC64;
         HSSP; P14687; 1AMU.

InterPro: IPR000873; AMP-bind.

InterPro: IPR0010873; AMP-bind.

InterPro: IPR0010880; Ppantne_attach.

Pfam; PF00501; AMP-binding; 4.

Pfam; PF00550; pp-binding; 4.

PROSITE: PS00012; PHOSPHOPANIN; 4.

PROSITE: PS00012; PHOSPHOPANING; 4.

PROSITE: PS00012; PHOSPHOPANIETHEINE; UNKNOWN_3.

Phosphopantetheine.

SEQUENCE 4379 AA; 491434 MM; 089F97BFC59BEA84 C
                                                                                                                                                                                                                12.2%; Score 1974; DB 2;
llarity 21.5%; Pred. No. 2.1e-112;
Conservative 614; Mismatches 1294;
AAF15891.2;
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Matches 847; Conserv
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                                                                                                                                                                                                                   MQKAFLFDHTTARPRPF-VPFYIDFPSTSEPDAAGLIKACESLVNHLDIFRTVFAEASGE
                                                                                                                                                                                                                                                                                                                                                                                                             :|| : ::: : | : || || : ::: | || || || ETKHI-LLVCMHHIVSDGWSMSVFLQELAALYNACSQAQTSPLAPLPIQYADFALWQRQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQGDVLQSQLSYWQQQLKDAPALLSLPTDRPRGPVQTFAGGHQEFALSVELSNKLTKLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLRGSSNIITQATVFNAACALVLSRESDSKDVVFGRIVSGRQGLPVEYQDIVGPCTNAVP
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                                                                                                                                                                                                  2604 CDEFAKVLGFQ-VGITDNFFDLGGHSLMATKLAVRIGHRLDTTVSVKDVFDHPVLFQLAI
                                                                                                                                                                                                                                                                 ALDNLVQSKTNEIVGGREMAEYSPFQLLFTEDPEEFMASEIKPQLELQEIIQDIYP-STQ
                                                                                                                                                                                                                                                                                                                                                  | : : | : : | : : | : : | : : | : : | CQRLWFLDQFEPNSAIYNIPMALRLVGTL--NQVALEQSLYEIINRHEALRTNFVTVNGK
                                                                                                                                                                                                                                                                                                                                                                                        LYQVVLSCLDLPIQVI - - - - - - - - TEDNINTATNEFLDEFAKEPVRLGH - PLIRFT - - IIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TADGRESGHGFWRDVIQNTP--MTILSD-----DTVVDGNDATCKALHLSKIVNIPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2541 MRTINLAGNPSFSELLGRVREMAMEAYTYQNLPFEML-----VEALQ-----PHRDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHP--ESQFEQQRVEM-----GVLTKFVNIEMDEPLYDLAIAGEVEPDGAGLKVTVIAK
                RGSDLLTNRPLQRLQNRRIAIEVRERLRSLLPSYMIPSNIVVLDKMPLNANGKVDRKELS
                                                                            RRAKVVPKQQTAAPLPTFPISEVEVILCEEATEVFGMKVDITDHFFNLGGHSLLATKLIS
                                                                                                                                      2544 RIDQRLKVRITVKDVFDHPVFADLASVIRQGLGLQQPVSDGQGQDRSAHMAPRTETEAIL
                                                                                                                                                                      -----KYVAPRTPIEEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTKSMRVIMRISHALYDGLSLEHVVRKLHMLYNGRS-----LLP-PHQFSRYMQY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-GSV224;
Hoffmann D., Hevel J.M., Moore R.E.;
"Characterization of the nostopeptolide biosynthetic gene cluster of Nostoc sp. GSV224.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                 Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                      Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
NCBI_TaxID=76334;
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                                                                                                     -----ALPKP-----
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1		Dp	1834 PVELQ ERFFARLECELHNLYGP
qq	830 QGYFNRPELTKEKFIPNPFEKAGSRRQERGGRRQKVEGSKLYKTGDLARYLA 881	ò	1894 YVVDPEOOLVGIGVMGELVVTGD
oy .	874 DGSIVCLGRIDSQVKIRGQRVELGAIETHLRQQMPDDLTIVVEATKRSQSANSTSLIAFL 933	op qu	
QQ	882 DGNIEYLGRIDNQVKIRGFRIELSEIEAVLSQHGDVQVSCVIVREDTPGDKRLVAYV 938	ΔO	1937 VNDOTVKAYRTGDRVRYRI
Qy	YFGNRPSDAHILDHDATKAINIKLEOVLPRHSIPSFYICMLELPRTATGKID	qq	
qa .		Qy	1993 RDAAVVLQQNEDQAPEILGFVVA
yo e	990 RRRLKIMGKDILDKOTOGAIVOQAPAPIPVFADTAAKLHSIWVQSLGIDPATVNVGATFF 1049	QQ	: :  : :: :: :: : : :
3 6		Qy	2022NDK
Š 2	1030 ELGGNOITALKÄVNMAKSY-GMDLKYSNIIQHFTLAGISAVKGDPLSYTLIFKS 1103    -  -  -  -	qq	11 2066 TSNGKVDRRALPAPDLSSEIKDK
}		Qy	2025
3 2	THE CONTROL OF THE TRANSPORT OF THE TANK OF THE CONTROL OF THE CON	QQ	2126 SLLATQLVSRIRNIFKVELPLRE
3 8		Qy	2036DHFE
S 8	11 ELGOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Db	2186 LALSYAQORLWFLDQFEPNSPFY
l è	ENL SSRAGWRATI LEIGEDDHII TIVMHHII SDGWSI DWI BRDI NOI WSAAI KDSKDPI S	Qy	2040
7 E		qa	2246 VDGQATQIIQTETNWTVSIVDLK
3 8	· (	Ολ	2040
Š	1209 ALIFLETQISDEANMQIN-"CFIEGENCHNIWANGLANS-SPANIFIUFAKKALLSGUAG 1323	Db	2306 LSETEHILLMCIHHIVSDGWSIG
3 ;	SLARE LE LE LA FALMERT MAN DE LA LA LA LA LA LA LA LA LA LA LA LA LA	Qy	2065 YDGSQIDFDEMHEWLG
Š €	1320 CVHVIIDGELIQSERAFCNEHNTISE VULAAR KAARIKLIRVEDAVIGIT LANKNRREL 1383 1327 VORDA GARITOET DOI GOROOTUMI IARDENTI VERHAARDIT VORDIANDEET 1306	qq	: ::   2366 WLQGEVLQSQLSYWQQKLASAPT
2 6	IQNFALSABLIGKLIGUSQAQGVILFMILLAAAFUILLINIIOAEDILAVGSFIANKUKSEI	Qy	2100 TGSGMILFNLDSRLESYV
ද් දි	1380 EDIIGCEVNIQUAKINLUHHUFEGILINQVARITIAAFENEDIFERNVSALQFGSKOLS 1445   :                :: :    : :   : :     :	Db	:
3 8	THE PROPERTY OF CHEMISTRY OF THE PROPERTY CHEMISTRY CHEM	Qy	2153IGQVDDL
S &		Оb	2486 GNPSFSELLGRVREMAMEAYSHQ
3 8		QY	2177
3 8	15.05 DEPARTMENT OF THE TRANSPORT OF THE	QQ	2546 ELTGLTVSSLPIKGTTSRFDLTL
ì		Qy	2179
Z qa		QO	2606 GIIANPEERISQLPLLTQLEQQK
č	7697	ΟŊ	2191 -NVQRIFFGDVRSQATNEHFLAA
5. E		QQ	2666 RSANAVVFEDQQLTYYELNYRAN
3 6		QY	2234LEDM
7 d	1669 OI.KEKI.POHOGOVVCI.DTDMORTSOSSORNI.TTTVOASNI.XVITYTGGSTGKPKGAMNTH 1728	QQ	2726 GAAYVPLDPEYPPERLSFILEDA
}		Qy	2275 LSAYRYAAVVHVRG
7 A	MQQAYQLTALDCILQKTPFSFDVSVWEFFWPLITGARLVVAK	QQ	
Qy	VTSSS	δλ	2314 KS
qa		QO	ASINFDVSFQEIFT
		Qy	2337ITAFERQV

Qy	4 (	TESFINGVPIGRALNNSGA 18
a &	1894	LKIVFIGRAIANIQI 188
6 6	0	REVGEOGSKGAKIL 194
Qy	1937	RIGDGLIEFFGRMDTQFKIRGNRIESAEIEAALLRDSSV
Dp	1948	PNSQSLVPNPQLYKTGDLARY-LPDGTIEYIGRIDNQVKIRGFRIELGEIEVLLNQCEDV 2006
Qy	1993	RDAAVVLQQNEDQAPEILGEVVADHDHSE2021
Dp	2007	QASCVIAREGTTGDKCLVAYVV-PHQHSKPTTNELRQFLKAKLPDYMVPSAFVILESMPL 2065
Qy	2022	2024
qq	2066	1   TSNGKVDRRALPAPDLSSEIKDKYVAPRTPIEEMLAQTWSQVLQLPQVGIHDNFFELGGH 2125
Qy	2025	
qq	2126	SILATQLVSRIRNIFKVELPLRELFAAATLAELAREIEQLQQQDLQLSAPPILPRAENAQ 2185
Qy	2036	2039
pp	2186	LALSYAQORLWFLDOFEPNSPFYNMSIALRLAGTVEVAALEQSFQOIIHRHEALRTNFIT 2245
Qy	2040	2039
qa	2246	VDGQATQIIQTETNWTVSIVDLKNLSTTKQEIASQQLVQQQAIQPFELATQALVRATLVV 2305
Qy	2040	SGMYSDIGEIDPSTIGSDFKGWISM 2064
qq	2306	LSETEHILLMCIHHIVSDGWSIGLFLQELAALYNAYSQGKSSTLAPLPIQYADFALWQRQ 2365
Qy	2065	YDGSQIDFDEMHEWLGGNVLEIG 2099
qa	2366	WLQGEVLQSQLSYWQQKLASAPTLLSLPTDRPRPSVQTYQGTHQEFALSEELTGKLAKLS 2425
Oy	2100	NLDSRLESYVGLEPSRSAA
qq	2426	OEQCYTLFWTLLAAFDTLLYRYTGTEDILVGSPIANRDRSEIEGLIGFFVNTLVMRTDLS 2485
Qy	2153	dн
qq	2486	GNPSFSELLGRVREMAMEAYSHQHLPFEMLVEALQPERDLSHSPLFQVMFVLQNAPTSGL 2545
Qy	2177	2178
QQ	2546	ELTGLTVSSLPIKGTTSRFDLTLIMQNSPTGLIGVWEYNTDLFDASTIERMTGHFVTLLE 2605
QY	2179	2190
qq	2606	GIIANPEERISQLPLLTQLEQQKLLVEWNDTQVDYPQDLCIHQLFEKQVDSTPDAIALIA 2665
Qy	2191	-NVORIFEGDVRSQATNEHFLAARAIHTLGKNATKDDVRQKMAE 2233
qq	2666	RSANAVVFEDQQLTYYELNYRANQLAHYLQSLGVGSDALVGLCVERSLEMVIGLLGILKA 2725
Qy	2234	AFF
QQ	2726	GAAYVPLDPEYPPERLSFILEDAQVSVLLTQQSILDRLPQHQANQVCLDTDAQLISQ 2782
Qy	2275	LSAYRYAAVVHVRGSLGDELVLPVEKDDWIDFQANQLNQ 2313
Dp	2783	CSQDNLISDVQANNLAYIIYTSGSTGQPKGIAMNQLALSNLILWHRENLKIPRGAKTLQF 2842
Qy	2314	KSAVSK-IPFE 2336
QQ	2843	ASINFDVSFQEIFTTWCSGGTLFLIGEELRRDTSALLGFLQQKAIERMFLPFVALQQLAE 2902
Qy	2337	ITAFERQVVASLNSN 2351

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LVTDGSHVNNGINGFLQQ----ITESSHFMPCNNRALLLHCQMESSGALL---VAYYDHN 433
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                                                                                                                                                                Saito F., Hori K., Kanda M., Kurotsu T., Saito Y.; "Entire nucleotide sequence for Bacillus brevis Nagano grs2 gene encoding gramicidin S synthetase 2; a multifunctional peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 1098;
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                   Bacillales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PRO0154, AMPBINING.
PROSITE, PRO0155, ACP_DOMAIN, 4.
PROSITE, PS00075, ALDEHVDE_DEHVDR_CYS; UNKNOWN_2.
PROSITE; PS000455, AMP_BINDING; 4.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_4.
SEQUENCE 4450 AA; 508674 MW; F3197E77BF69316D CRC64;
    Bacteria; Firmicutes; Bacillus/Clostridium group;
Paenibacillaceae; Brevibacillus.
NCBI_TaxID=1393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.0%; Score 1933; DB 2; Best Local Similarity 22.0%; Pred. No. 7.7e-110; Matches 845; Conservative 587; Mismatches 1306;
                                                                                                                                                                                                                           synthetas.";

J. Biochem. 116:357-367(1994).

EMBL: D29676; BAA06146.1;

HSSP; P14687; 1AMU.

InterPro: IPR0012086, Aldehyde_dehydr.

InterPro: IPR0012086; AMP-bind.

InterPro: IPR001242; Condensatn.

InterPro: IPR001242; Condensatn.

InterPro: IPR001380; Ppantue_attach.

InterPro: IPR000379; Ser_estrs.

InterPro: IPR00131; Thioesterase.
                                                                                                                                            MEDLINE=95122465; PubMed=7822255;
Saito F., Hori K., Kanda M., Kuro
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Pfam; PF00668; Condensation; 4.
Pfam; PF00550; pp-binding; 4.
Pfam; PF00575; Thioesterase; 1.
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                                                                                              VETWPLLPPVGRPIANAQIYILDRFLQPVPVGVPGELYIAGVLLSQGYFNRPELTLEKFI
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STRAIN-8A3(2) / M145;
STRAIN-8A3(2) / M145;
STRAIN-8A3(2) / M145;
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kleeser H.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kleeser H.,
Harper D., Bateman A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleeser T., Larke L., Murphy L., Oliver K., O'Nell S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wletzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycesaciosics: Streptomyces.
NCBL_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 3670;
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to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol, 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDA peptide synthetase II.
CDAPS2 OR SC03231 OR SCE63.02C.
Streptomyces coelicolor.
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3670 AA
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InterPro; IPR001242; Condensatn.
InterPro; IPR003880; Ppantne_attach.
Pfam; PF00501; AMP-binding; 3.
Pfam; PF00568; Condensation; 4.
Pfam; PF00550; pp-binding; 3.
PROSITE; PS50075; ACP_DOWAIN; 3.
PROSITE; PS00455; AMP_BINDING; 2.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UN
PRT;
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MEDLINE=97000351; PubMed=8843436;
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EMBL; AL035640; CAB38517.1; -.
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PRELIMINARY;
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Saunder D.C., Harris
Submitted (MAR-1999)
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Bentley S.D.,
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IV -- HEKLSEEMKVIDLCGSDL 1195 || | :: |:|: |VLPVEAVATPFAVVDVAAEDV 1123 VMHHIISDGWSIDVLRRDLNQL 1255 KFQGLESVPVPSKAYT-RFDME 1486
:| || : | || : || || RFAGLAAEVVASESVSARFDLS 1417 -----KQLNYWKKQLKD-SSP 1307 :|| |||:|| PDTLAGRQLAYWKQQLAGLPEQ 1238 HNTTSFVVLLAAFRAAHYRLTA 1367 |||:|:|:|| | | | TNTTAFMVIQAALAALLTRHGA 1298 DTFGTLINQVKATTTAAFENED 1427 || | | ::| | |::| PTFRDLLTRVRDTDLTAYTHQD 1358 FFEILRNGLQSSRTPVSILPLT 1540 PSETRMAHMATIAFDGASYEIY 1770 VMGELVVTGDGLARGXSDK-AL 1927 | ||| :|| :|| :|| | PGELXLAGEQLAQGYHLRPAL 1839 MDTQFKIRGNRIESAEIEAALL 1987 :| | | |:|| ||| || || | VDQQVKLRGFRIELGEIEAELS 1898 ::||| || || || :|| LVHHIASDAWSRGPLAQDLTAA 1181 CVRLLAAAVAHPGRSVGQLEIM 1477 SLAVVDSSCRLTYTELDRQSDI 1600 : |: ||: ||:| ||: |:: ATALEFGEVRLSYAELNARANR 1536 AYLPLDVRSPSARVQDILSGLS 1660 |||||:| |: ||: :|: : AYLPIDPHYPADRVEYMLAD-A 1595 EVIEHDSTKPSATSLAYVLYTS 1720 [-----SSSQDV 1815 SLYQGVQCYNGYGPTENGVMST 1868 : | ||||| ::| ---RARSVINLYGPIEATIWAT 1784 SANQVEGWQDHFESGMYSDIG 2047 PHYQATPSLWQGVAAVAGDELA 1744 HDNRSLGNVLEIGTGSGMILF 2107 OVGTATDIGQVDDLHPDLVVLN 2167 2168 SVIQYFPSSEYLAEIADTLIHLPNVQRIFFGDVRSQATNEHFLAARAIHTLGKNATKDDV 2227 ô

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